

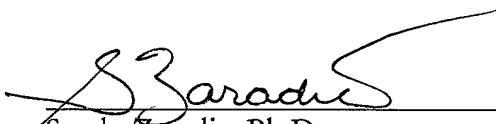
Applicant's Reference: DX01170K US

Title of Invention: MAMMALIAN RECEPTOR PROTEINS;
RELATED REAGENTS AND METHODS

Applicant: Daniel M. Gorman

Sequence Listing Statement

The undersigned agent for applicant hereby declares that the information recorded on the diskette is identical in content to the information in the written Sequence Listing.


Sandy Zaradic, Ph.D.
Patent Agent
Registration No. 45,997

Date: May 22, 2001

09563818 052201

SEQUENCE SUBMISSION

SEQ ID NO: 1 is primate DCRS6 nucleotide sequence.
 SEQ ID NO: 2 is primate DCRS6 polypeptide sequence.
 SEQ ID NO: 3 is primate DCRS6 reverse translation.
 SEQ ID NO: 4 is rodent DCRS6 nucleotide sequence.
 SEQ ID NO: 5 is rodent DCRS6 polypeptide sequence.
 SEQ ID NO: 6 is rodent DCRS6 reverse translation.
 SEQ ID NO: 7 is primate DCRS7 nucleotide sequence.
 SEQ ID NO: 8 is primate DCRS7 polypeptide sequence.
 SEQ ID NO: 9 is primate DCRS7 reverse translation.
 SEQ ID NO: 10 is rodent DCRS7 nucleotide sequence.
 SEQ ID NO: 11 is rodent DCRS7 polypeptide sequence.
 SEQ ID NO: 12 is rodent DCRS7 reverse translation.
 SEQ ID NO: 13 is primate DCRS8 nucleotide sequence.
 SEQ ID NO: 14 is primate DCRS8 polypeptide sequence.
 SEQ ID NO: 15 is primate DCRS8 reverse translation.
 SEQ ID NO: 16 is primate DCRS9 nucleotide sequence.
 SEQ ID NO: 17 is primate DCRS9 polypeptide sequence.
 SEQ ID NO: 18 is primate DCRS9 reverse translation.
 SEQ ID NO: 19 is rodent DCRS9 nucleotide sequence.
 SEQ ID NO: 20 is rodent DCRS9 polypeptide sequence.
 SEQ ID NO: 21 is rodent DCRS9 reverse translation.
 SEQ ID NO: 22 is primate DCRS10 nucleotide sequence.
 SEQ ID NO: 23 is primate DCRS10 polypeptide sequence.
 SEQ ID NO: 24 is primate DCRS10 reverse translation.
 SEQ ID NO: 25 is rodent DCRS10 nucleotide sequence.
 SEQ ID NO: 26 is rodent DCRS10 polypeptide sequence.
 SEQ ID NO: 27 is rodent DCRS10 reverse translation.
 SEQ ID NO: 28 is primate IL-17 receptor peptide sequence.
 SEQ ID NO: 29 is rodent IL-17 receptor peptide sequence.
 SEQ ID NO: 30 is worm IL-17 receptor peptide sequence.
 SEQ ID NO: 31 is worm DCRS6 nucleotide sequence.

<110> Gorman, Daniel M.

<120> Mammalian Receptor Proteins; Related Reagents and Methods

<130> DX01170K US

<140>

<141>

<150> US 60/206,862

<151> 2000-05-24

<160> 31

<170> PatentIn Ver. 2.0

<210> 1

<211> 1796

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised Homo sapiens

09863818 "0599441

<222> (4) .. (1509)

<222> (46) .. (1509)

gcg atg tcg ctc gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc 48
Met Ser Leu Val Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala
-10 -5 -1 1

gta ccc cga gag ccg acc gtt caa tgt ggc tct gaa act ggg cca tct 96
Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser
5 10 15

cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac 144
Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp
20 25 30

ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca 192
Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser
35 40 45

att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc cgc 240
Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg
50 55 60 65

ttg	ttg	aag	gcc	acc	aag	att	tgt	gtg	acg	ggc	aaa	agc	aac	ttc	cag	288
Leu	Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	
				70					75					80		

tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag 336
Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln
85 90 95

acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct 384
Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro
100 105 110

gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat 432
Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn
115 120 125

gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca 480
Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser
130 135 140 145

cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc aag 528
Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys
150 155 160

gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag 576
Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu
165 170 175

gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga tac 624
Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr
180 185 190

atg Met	gct Ala	ctt Leu	atc Ile	caa Gln	cac His	agc Ser	act Thr	atc Ile	atc Ile	ggg Gly	ttt Phe	tct Ser	cag Gln	gtg Val	ttt Phe	672
195200205																
gag Glu	cca Pro	cac His	cag Gln	aag Lys	aaa Lys	caa Gln	acg Thr	cga Arg	gct Ala	tca Ser	gtg Val	gtg Val	att Ile	cca Pro	gtg Val	720
210215220225																
act Thr	ggg Gly	gat Asp	agt Ser	gaa Glu	ggg Gly	gct Ala	acg Thr	gtg Val	cag Gln	ctg Leu	act Thr	cca Pro	tat Tyr	ttt Phe	cct Pro	768
230235240																
act Thr	tgt Cys	ggc Gly	agc Ser	gac Asp	tgc Cys	atc Ile	cga Arg	cat His	aaa Lys	gga Gly	aca Thr	gtt Val	gtg Val	ctc Leu	tgc Cys	816
245250255																
cca Pro	caa Gln	aca Thr	ggc Gly	gtc Val	cct Pro	ttc Phe	cct Pro	ctg Leu	gat Asp	aac Asn	aac Asn	aaa Lys	agc Ser	aag Lys	ccg Pro	864
260265270																
gga Gly	ggc Gly	tgg Trp	ctg Leu	cct Pro	ctc Leu	ctc Leu	ctg Leu	ctg Leu	tct Ser	ctg Leu	ctg Leu	gtg Val	gcc Ala	aca Thr	tgg Trp	912
275280285																
gtg Val	ctg Leu	gtg Val	gca Ala	ggg Gly	atc Ile	tat Tyr	cta Leu	atg Met	tgg Trp	agg Arg	cac His	gaa Glu	agg Arg	atc Ile	aag Lys	960
290295300305																
aag Lys	act Thr	tcc Ser	ttt Phe	tct Ser	acc Thr	acc Thr	aca Thr	cta Leu	ctg Leu	ccc Pro	ccc Pro	att Ile	aag Lys	gtt Val	ctt Leu	1008
310315320																
gtg Val	gtt Val	tac Tyr	cca Pro	tct Ser	gaa Glu	ata Ile	tgt Cys	ttc Phe	cat His	cac His	aca Thr	att Ile	tgt Cys	tac Tyr	ttc Phe	1056
325330335																
act Thr	gaa Glu	ttt Phe	ctt Leu	caa Gln	aac Asn	cat His	tgc Cys	aga Arg	agt Ser	gag Glu	gtc Val	atc Ile	ctt Leu	gaa Glu	aag Lys	1104
340345350																
tgg Trp	cag Gln	aaa Lys	aag Lys	aaa Lys	ata Ile	gca Ala	gag Glu	atg Met	ggg Gly	cca Pro	gtg Val	cag Gln	tgg Trp	ctt Leu	gcc Ala	1152
355360365																
act Thr	caa Gln	aag Lys	aag Lys	gca Ala	gca Ala	gac Asp	aaa Lys	gtc Val	gtc Val	ttc Phe	ctt Leu	ctt Leu	tcc Ser	aat Asn	gac Asp	1200
370375380385																
gtc Val	aac Asn	agt Ser	gtg Val	tgc Cys	gat Asp	ggg Gly	acc Thr	tgt Cys	ggc Gly	aag Lys	agc Ser	gag Glu	ggc Gly	agt Ser	ccc Pro	1248
390395400																
agt Ser	gag Glu	aac Asn	tct Ser	caa Gln	gac Asp	ctc Leu	ttc Phe	ccc Pro	ctt Leu	gcc Ala	ttt Phe	aac Asn	ctt Leu	ttc Phe	tgc Cys	1296
405410415																
agt Ser	gat Asp	cta Leu	aga Arg	agc Ser	cag Gln	att Ile	cat His	ctg Leu	cac His	aaa Lys	tac Tyr	gtg Val	gtg Val	gtc Val	tac Tyr	1344
420425430																

ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc 1392
 Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys
 435 440 445

ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt 1440
 Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu
 450 455 460 465

ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc 1488
 Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
 470 475 480

cac gat ggc tgc tgc tcc ttg tagccacccc atgagaagca agagacctta 1539
 His Asp Gly Cys Cys Ser Leu
 485

aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgacacctga agcttactat 1599

gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaaatt ttcaaataatt 1659

gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 1719

tatacataga aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca 1779

ataaagcatc ttcagcc 1796

<210> 2

<211> 502

<212> PRT

<213> Unknown

<400> 2

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
 -10 -5 -1 1

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 5 10 15

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 20 25 30

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 35 40 45 50

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 55 60 65

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 70 75 80

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
 85 90 95

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 100 105 110

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 115 120 125 130

056313 05301

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
 135 140 145
 Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
 150 155 160
 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 165 170 175
 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
 180 185 190
 Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 195 200 205 210
 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 215 220 225
 Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
 230 235 240
 Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
 245 250 255
 Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
 260 265 270
 Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
 275 280 285 290
 Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
 295 300 305
 Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
 310 315 320
 Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
 325 330 335
 Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
 340 345 350
 Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
 355 360 365 370
 Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
 375 380 385
 Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
 390 395 400
 Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
 405 410 415
 Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
 420 425 430
 Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
 435 440 445 450

05363818 "052301

```
<210> 3
<211> 1506
<212> DNA
<213> reverse translation
```

```

<400> 3
atgwsnytnng tnytnytnws nytngcngcn ytntgymgnw sngcngtncc nmngngarccn 60
acngtncart gyggnwsnga racnggnccn wsncngart ggatgytnca rcaygayytn 120
athccnggng ayytnmnga yytnmgngtn garccngtna cnacnwsngt ngcnacnggn 180
gaytaywsna thytnatgaa ygtnwsntgg gtynytnmgng cngaygcnws nathmgnytn 240
ytnaargcna cnaarathtg ygtnacnggn aarwsnaayt tycarwsnta ywsntgygtn 300
mgntgyaayt ayacngargc nttycaracn caracnmgnc cnwsnggngg naartggacn 360
ttywsntaya thggnttycc ngtngarytn aayacngtnt ayttyathgg ngcncayaay 420
athccnaayg cnaayatgaa ygargayggn ccnwsnatgw sngtnaaytt yacnwsnccn 480
ggntgyytnng aycayathat gaartayaar aaraartgyg tnaargcngg nwsnytnntgg 540
gayccnaaya thacngcntg yaaraaraay gargaracng tngargtnaa yttyacnacn 600
acnccnytnng gnaaymgnta yatggcnytn athcarcayw snacnathat hggnttywsn 660
cargtnnttyg arccncayca raaraarcar acnmngncnw sngtngtntat hccngtnacn 720
ggngaywsng arggngcnac ngtnrcarytn acnccntayt tyccnacntg yggnwsngay 780
tgyathmgnc ayaarggnac ngtngtnytn tgyccncara cnggngtncc nttyccnytn 840
gayaayaaya arwsnaarcc nggnggntgg ytnccnytny tnytnytnws nytnytnngtn 900
gcnacntggg tnytngtngc nggnathtay ytnatgtggm gncaygarmg nathaaraar 960
acnwsnttyw snacnacnac nytnytnccn ccnathaarg tnytngtngt ntayccnwsn 1020
garathtgyt tycaycayac nathtgytay ttyacngart tyytncaraa ycaytgygmgn 1080
wsngargtna thytngaraa rtggcaraar aaraarathg cngaratggg nccngtncar 1140

```

<210> 4
<211> 637
<212> DNA
<213> Unknown

```
<220>
<221> CDS
<222> (1)..(210)
```

<400>	4																
gat	ttc	agc	agc	cag	acg	cat	ctg	cac	aaa	tac	ctg	gag	gtc	tat	ctt	48	
Asp	Phe	Ser	Ser	Gln	Thr	His	Leu	His	Lys	Tyr	Leu	Glu	Val	Tyr	Leu		
1				5					10					15			
ggg	gga	gca	gac	ctc	aaa	ggc	gac	tat	aat	gcc	ctg	agt	gtc	tgc	ccc	96	
Gly	Gly	Ala	Asp	Leu	Lys	Gly	Asp	Tyr	Asn	Ala	Leu	Ser	Val	Cys	Pro		
			20					25					30				
caa	tat	cat	ctc	atg	aag	gac	gcc	aca	gct	ttc	cac	aca	gaa	ctt	ctc	144	
Gln	Tyr	His	Leu	Met	Lys	Asp	Ala	Thr	Ala	Phe	His	Thr	Glu	Leu	Leu		
		35					40					45					
aag	gct	acg	cag	agc	atg	tca	gtg	aag	aaa	cgc	tca	caa	gcc	tgc	cat	192	
Lys	Ala	Thr	Gln	Ser	Met	Ser	Val	Lys	Lys	Arg	Ser	Gln	Ala	Cys	His		
	50					55					60						
gat	agc	tgt	tca	ccc	ttg	tagtccaccc	gggggaatag	agactctgaa								240	
Asp	Ser	Cys	Ser	Pro	Leu												
65					70												
gccttcctac	tctcccttcc	agtgacaaat	gctgtgtgac			gactctgaaa			tgtgtgggag			300					
aggctgtgtg	gaggtagtgc		tatgtacaaa			cttgctttaa			aactggagtt			tgcaaagtca			360		
acctgagcat	acacgcctga			ggctagtcac			tggctggatt			tatgaagaca			acacagttac			420	
agacaataat		gagtgggacc			tacatttggg			atatacccaa			agctgggtaa			tgattatcac			480
tgagaaccac		gcactctggc			catgaggtaa			tacggcactt			ccctgtcagg			ctgtctgtca			540
ggttgggtct		gtcttgcaact			gcccattgctc			tatgctgcac			gtagaccqtt			ttqtaacatt			600

ttaatctgtt aatgaataat ccgtttggga ggctctc

637

<210> 5
<211> 70
<212> PRT
<213> Unknown

<400> 5
Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
1 5 10 15

Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
20 25 30

Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
35 40 45

Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
50 55 60

Asp Ser Cys Ser Pro Leu
65 70

<210> 6
<211> 210
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(210)
<223> n may be a, c, g, or t

<400> 6
gayttywsnw sncaracnca yytncayaar tayytnngarg tntayytnng ngngcngay 60
ytnaarggng aytayaaygc nytnwsngtn tgyccncart aycayytnat gaargaygcn 120
acngcnttyc ayacngaryt nytnaargcn acncarwsna tgwsngtnaa raarmgnwsn 180
cargcntgyc aygaywsntg ywsnccnytn 210

<210> 7
<211> 2308
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (181)..(2289)

<220>

09363348 "053301

<221> mat_peptide
<222> (241)..(2289)

<220>
<221> misc_feature
<222> (664)
<223> Xaa translation depends on genetic code

<400> 7
gagtcaggac tcccaggaca gagagtgcac aaactaccca gcacagcccc ctccgcccc 60
tctggaggct gaagagggat tccagcccct gccacccaca gacacgggct gactgggggtg 120
tctgcccccc ttggggggcan ccacagggcc tcaggcctgg gtgccacctg gcactagaag 180
atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag 228
Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
-20 -15 -10 -5
tgg atc ctt tct ctg gag agg ctt gtg ggg cct cag gac gct acc cac 276
Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
-1 1 5 10
tgc tct ccg ggc ctc tcc tgc cgc ctc tgg gac agt gac ata ctc tgc 324
Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
15 20 25
ctg cct ggg gac atc gtg cct gct ccg ggc ccc gtg ctg gcg cct acg 372
Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
30 35 40
cac ctg cag aca gag ctg gtg ctg agg tgc cag aag gag acc gac tgt 420
His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
45 50 55 60
gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg 468
Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
65 70 75
gaa gag cct gaa gat gag gaa aag ttt gga gga gca gct gac tta ggg 516
Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
80 85 90
gtg gag gag cct agg aat gcc tct ctc cag gcc caa gtc gtg ctc tcc 564
Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
95 100 105
ttc cag gcc tac cct act gcc cgc tgc gtc ctg ctg gag gtg caa gtg 612
Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
110 115 120
cct gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat 660
Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
125 130 135 140
gac tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat 708
Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
145 150 155
act cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct 756

09063815 "090301

Thr	Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro		
			160					165					170				
gac	tgc	agg	ggg	ctc	gaa	gtc	tgg	aac	agc	atc	ccg	agc	tgc	tgg	gcc	804	
Asp	Cys	Arg	Gly	Leu	Glu	Val	Trp	Asn	Ser	Ile	Pro	Ser	Cys	Trp	Ala		
		175					180					185					
ctg	ccc	tgg	ctc	aac	gtg	tca	gca	gat	ggg	gac	aac	gtg	cat	ctg	gtt	852	
Leu	Pro	Trp	Leu	Asn	Val	Ser	Ala	Asp	Gly	Asp	Asn	Val	His	Leu	Val		
	190					195					200						
ctg	aat	gtc	tct	gag	gag	cag	cac	ttc	ggc	ctc	tcc	ctg	tac	tgg	aat	900	
Leu	Asn	Val	Ser	Glu	Glu	Gln	His	Phe	Gly	Leu	Ser	Leu	Tyr	Trp	Asn		
205					210				215						220		
cag	gtc	cag	ggc	ccc	cca	aaa	ccc	cgg	tgg	cac	aaa	aac	ctg	act	gga	948	
Gln	Val	Gln	Gly	Pro	Pro	Lys	Pro	Arg	Trp	His	Lys	Asn	Leu	Thr	Gly		
			225					230						235			
ccg	cag	atc	att	acc	ttg	aac	cac	aca	gac	ctg	gtt	ccc	tgc	ctc	tgt	996	
Pro	Gln	Ile	Ile	Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	Leu	Cys		
			240					245					250				
att	cag	gtg	tgg	cct	ctg	gaa	cct	gac	tcc	gtt	agg	acg	aac	atc	tgc	1044	
Ile	Gln	Val	Trp	Pro	Leu	Glu	Pro	Asp	Ser	Val	Arg	Thr	Asn	Ile	Cys		
	255					260						265					
ccc	ttc	agg	gag	gac	ccc	cgc	gca	cac	cag	aac	ctc	tgg	caa	gcc	gcc	1092	
Pro	Phe	Arg	Glu	Asp	Pro	Arg	Ala	His	Gln	Asn	Leu	Trp	Gln	Ala	Ala		
	270					275					280						
cga	ctg	cga	ctg	ctg	acc	ctg	cag	agc	tgg	ctg	ctg	gac	gca	ccg	tgc	1140	
Arg	Leu	Arg	Leu	Leu	Thr	Leu	Gln	Ser	Trp	Leu	Leu	Asp	Ala	Pro	Cys		
285					290				295						300		
tgc	ctg	ccc	gca	gaa	gag	gca	ctg	tgc	tgg	cgg	gct	ccg	ggg	ggg	gac	1188	
Ser	Leu	Pro	Ala	Glu	Ala	Ala	Leu	Cys	Trp	Arg	Ala	Pro	Gly	Gly	Asp		
			305					310					315				
ccc	tgc	cag	cca	ctg	gtc	cca	ccg	ctt	tcc	tgg	gag	aat	gtc	act	gtg	1236	
Pro	Cys	Gln	Pro	Leu	Val	Pro	Pro	Leu	Ser	Trp	Glu	Asn	Val	Thr	Val		
		320						325					330				
gac	gtg	aac	agc	tgc	gag	aag	ctg	cag	ctg	cag	gag	tgc	ttg	tgg	gct	1284	
Asp	Val	Asn	Ser	Ser	Glu	Lys	Leu	Gln	Leu	Gln	Glu	Cys	Leu	Trp	Ala		
		335				340						345					
gac	tcc	ctg	ggg	cct	ctc	aaa	gac	gat	gtg	cta	ctg	ttg	gag	aca	cga	1332	
Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu	Thr	Arg		
	350					355					360						
ggc	ccc	cag	gac	aac	aga	tcc	ctc	tgt	gcc	ttg	gaa	ccc	agt	ggc	tgt	1380	
Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys		
365				370				375							380		
act	tca	cta	ccc	agc	aaa	gcc	tcc	acg	agg	gca	gct	cgc	ctt	gga	gag	1428	
Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu		
			385					390						395			
tac	tta	cta	caa	gac	ctg	cag	tca	ggc	cag	tgt	ctg	cag	cta	tgg	gac	1476	

09863818 "052304"

Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp		
			400					405					410				
gat	gac	ttg	gga	gcg	cta	tgg	gcc	tgc	ccc	atg	gac	aaa	tac	atc	cac	1524	
Asp	Asp	Leu	Gly	Ala	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His		
		415					420					425					
aag	cgc	tgg	gcc	ctc	gtg	tgg	ctg	gcc	tgc	cta	ctc	ttt	gcc	gct	gcg	1572	
Lys	Arg	Trp	Ala	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Phe	Ala	Ala	Ala		
	430					435					440						
ctt	tcc	ctc	atc	ctc	ctt	ctc	aaa	aag	gat	cac	gcg	aaa	ggg	tgg	ctg	1620	
Leu	Ser	Leu	Ile	Leu	Leu	Leu	Lys	Lys	Asp	His	Ala	Lys	Gly	Trp	Leu		
445					450					455					460		
agg	ctc	ttg	aaa	cag	gac	gtc	cgc	tcg	ggg	gcg	gcc	gcc	agg	ggc	cgc	1668	
Arg	Leu	Leu	Lys	Gln	Asp	Val	Arg	Ser	Gly	Ala	Ala	Ala	Arg	Gly	Arg		
			465					470						475			
gcg	gct	ctg	ctc	ctc	tac	tca	gcc	gat	gac	tcg	ggt	ttc	gag	cgc	ctg	1716	
Ala	Ala	Leu	Leu	Leu	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Phe	Glu	Arg	Leu		
		480					485					490					
gtg	ggc	gcc	ctg	gcg	tcg	gcc	ctg	tgc	cag	ctg	ccg	ctg	cgc	gtg	gcc	1764	
Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Cys	Gln	Leu	Pro	Leu	Arg	Val	Ala		
	495					500					505						
gta	gac	ctg	tgg	agc	cgt	cgt	gaa	ctg	agc	gcg	cag	ggg	ccc	gtg	gct	1812	
Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	Gln	Gly	Pro	Val	Ala		
	510				515					520							
tgg	ttt	cac	gcg	cag	cgg	cgc	cag	acc	ctg	cag	gag	ggc	ggc	gtg	gtg	1860	
Trp	Phe	His	Ala	Gln	Arg	Arg	Gln	Thr	Leu	Gln	Glu	Gly	Gly	Val	Val		
525				530				535						540			
gtc	ttg	ctc	ttc	tct	ccc	ggt	gcg	gtg	gcg	ctg	tgc	agc	gag	tgg	cta	1908	
Val	Leu	Leu	Phe	Ser	Pro	Gly	Ala	Val	Ala	Leu	Cys	Ser	Glu	Trp	Leu		
			545			550							555				
cag	gat	ggg	gtg	tcc	ggg	ccc	ggg	gcg	cac	ggc	ccg	cac	gac	gcc	ttc	1956	
Gln	Asp	Gly	Val	Ser	Gly	Pro	Gly	Ala	His	Gly	Pro	His	Asp	Ala	Phe		
		560				565						570					
cgc	gcc	tcg	ctc	agc	tgc	gtg	ctg	ccc	gac	ttc	ttg	cag	ggc	cgg	gcg	2004	
Arg	Ala	Ser	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln	Gly	Arg	Ala		
	575					580					585						
ccc	ggc	agc	tac	gtg	ggg	gcc	tgc	ttc	gac	agg	ctg	ctc	cac	ccg	gac	2052	
Pro	Gly	Ser	Tyr	Val	Gly	Ala	Cys	Phe	Asp	Arg	Leu	Leu	His	Pro	Asp		
	590				595			600									
gcc	gta	ccc	gcc	ctt	ttc	cgc	acc	gtg	ccc	gtc	ttc	aca	ctg	ccc	tcc	2100	
Ala	Val	Pro	Ala	Leu	Phe	Arg	Thr	Val	Pro	Val	Phe	Thr	Leu	Pro	Ser		
605				610				615						620			
caa	ctg	cca	gac	ttc	ctg	ggg	gcc	ctg	cag	cag	cct	cgc	gcc	ccg	cgt	2148	
Gln	Leu	Pro	Asp	Phe	Leu	Gly	Ala	Leu	Gln	Gln	Pro	Arg	Ala	Pro	Arg		
			625			630							635				
tcc	ggg	cgg	ctc	caa	gag	aga	gcg	gag	caa	gtg	tcc	cgg	gcc	ctt	cag	2196	

Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
640 645 650

cca gcc ctg gat agc tac ttc cat ccc ccg ggg acn tcc gcg ccg gga 2244
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly
655 660 665

cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act 2289
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
670 675 680

taaataaagg cagacgctg 2308

<210> 8
<211> 703
<212> PRT
<213> Unknown

<400> 8
Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
-20 -15 -10 -5

Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
-1 1 5 10

Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
15 20 25

Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
30 35 40

His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
45 50 55 60

Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
65 70 75

Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
80 85 90

Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
95 100 105

Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
110 115 120

Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
125 130 135 140

Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
145 150 155

Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
160 165 170

Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala
175 180 185

Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val

05663313 "0566301

190	195	200
Leu Asn Val Ser Glu	Glu Gln His Phe Gly	Leu Ser Leu Tyr Trp Asn
205	210	215 220
Gln Val Gln Gly	Pro Pro Lys Pro Arg	Trp His Lys Asn Leu Thr Gly
	225	230 235
Pro Gln Ile Ile Thr	Leu Asn His Thr Asp	Leu Val Pro Cys Leu Cys
	240	245 250
Ile Gln Val Trp Pro	Leu Glu Pro Asp Ser	Val Arg Thr Asn Ile Cys
	255	260 265
Pro Phe Arg Glu Asp	Pro Arg Ala His Gln	Asn Leu Trp Gln Ala Ala
	270	275 280
Arg Leu Arg Leu Leu	Thr Leu Gln Ser Trp	Leu Leu Asp Ala Pro Cys
	285	290 295 300
Ser Leu Pro Ala Glu	Ala Ala Leu Cys Trp	Arg Ala Pro Gly Gly Asp
	305	310 315
Pro Cys Gln Pro Leu	Val Pro Pro Leu Ser	Trp Glu Asn Val Thr Val
	320	325 330
Asp Val Asn Ser Ser	Glu Lys Leu Gln Leu	Gln Glu Cys Leu Trp Ala
	335	340 345
Asp Ser Leu Gly Pro	Leu Lys Asp Asp Val	Leu Leu Leu Glu Thr Arg
	350	355 360
Gly Pro Gln Asp Asn	Arg Ser Leu Cys Ala	Leu Glu Pro Ser Gly Cys
	365	370 375 380
Thr Ser Leu Pro Ser	Lys Ala Ser Thr Arg	Ala Ala Arg Leu Gly Glu
	385	390 395
Tyr Leu Leu Gln Asp	Leu Gln Ser Gly Gln	Cys Leu Gln Leu Trp Asp
	400	405 410
Asp Asp Leu Gly Ala	Leu Trp Ala Cys Pro	Met Asp Lys Tyr Ile His
	415	420 425
Lys Arg Trp Ala Leu	Val Trp Leu Ala Cys	Leu Leu Phe Ala Ala Ala
	430	435 440
Leu Ser Leu Ile Leu	Leu Leu Lys Lys Asp	His Ala Lys Gly Trp Leu
	445	450 455 460
Arg Leu Leu Lys Gln	Asp Val Arg Ser Gly	Ala Ala Ala Arg Gly Arg
	465	470 475
Ala Ala Leu Leu Leu	Tyr Ser Ala Asp Asp	Ser Gly Phe Glu Arg Leu
	480	485 490
Val Gly Ala Leu Ala	Ser Ala Leu Cys Gln	Leu Pro Leu Arg Val Ala
	495	500 505
Val Asp Leu Trp Ser	Arg Arg Glu Leu Ser	Ala Gln Gly Pro Val Ala

510 515 520
 Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val
 525 530 535 540
 Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu
 545 550 555
 Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
 560 565 570
 Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala
 575 580 585
 Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
 590 595 600
 Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser
 605 610 615 620
 Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
 625 630 635
 Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
 640 645 650
 Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly
 655 660 665
 Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
 670 675 680

<210> 9
 <211> 2109
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(2109)
 <223> n may be a, c, g, or t

<400> 9
 atgccngtnc cntgggttyt nytnwsnytn gcnytnnggm gnwsncartg gathytnwsn 60
 ytnrgarmgny tngtnggncc ncargaygc acncaytgyw snccnggnyt nwsntgymgn 120
 ytnrtgggayw sngayathyt ntgyytnccn ggngayathg tncngcncc nggncngtn 180
 ytnngcnccna cncayytnca racngarytn gtynnmngt gycaraarga racngaytgy 240
 gayytnrtgyy tnmngntngc ngtncayytn gcngtncayg gncaytggga rgarcngar 300
 gaygargara arttyggngg ngcngcngay ytnngngtng argarcnmg naaygcwnsn 360
 ytnrcargcnc argtngtnyt nwsnttycar gcntayccna cngcnmgntg ygtnytnytn 420
 gargtnrcarg tncngcngc nytngtncar ttyggncarw sngtnggnws ngtngtntay 480

05863318 "05863301"

gaytgyttyg argcngcny t nggnwsngar gtnmgnatht ggwsntayac ncarccnmgn 540
 taygaraarg arytnaayca yacncarcar ytncngayt gymngggny t ngargtntgg 600
 aaywsnathc cnwsntgytg ggcnytnccn tggytnaayg tnwsngcnga yggngayaay 660
 gtncayytng tnytnaaygt nwsngargar carcayttyg gnytnwsnyt ntaytggaay 720
 cargtncarg gncncncnaa rccnmgttg cayaaraay tncnggncc ncarathath 780
 acnytnaayc ayacngayt ngtnccntgy ytntgyathc argtntggcc nytngarccn 840
 gaywsngtnm gnacnaayat htgyccntty mgngargayc cnmgngcnca ycaraayytn 900
 tggcargcng cnmgnytnmg nytnytnacn ytncarwsnt ggytnytnga ygcncntgy 960
 wsnytnccng cngargcngc nytnygytg mgngcncng gngngaycc ntgycarccn 1020
 ytngtnccnc cnytnwsntg ggaraaygt acngtngayg tnaaywsnws ngaraarytn 1080
 carytncarg artgyytn t ggengaywsn ytnggncny tnaargayga ygtnytnytn 1140
 ytngaracnm gnggncnca rgayaaymgn wsnytnygy cnytngarcc nwsnggntgy 1200
 acnwsnytn cwnsnaargc nwsnacnmgn gcngcnmgny tngngarta yytnytnear 1260
 gayytnearw snggncartg yytnarytn tgggaygay ayytnggngc nytntgggcn 1320
 tgyccnatgg ayaartayat hcayaarmgn tgggcnytng tntggytngc ntgyytnytn 1380
 ttygcngcng cnytnwsnyt nathytnytn ytnaaraarg aycaygcnaa rggntggytn 1440
 mgnytnytna arcargaygt nmgnwsnggn gcngcngcnm gnggnmgngc ngcnytnytn 1500
 ytntaywsng cngaygayws nggnttygar mgnytngtng gngcnytnge nwsngcnytn 1560
 tgyarytn cnytnmgngt ngcngtngay ytntggwsnm gnmngaryt nwsngcncar 1620
 gngcngtng cntggttyca ygencarmgn mgncaracny tncargargg nggngtngtn 1680
 gtnytnytn tywsnccng ngcngtngcn ytntgywsng artggytnca rgayggngtn 1740
 wsnggncng gngcncaygg nccncaygay gcnttymgng cwnsnytnws ntgygtnytn 1800
 cengaytty tncarggnmg ngcncnggn wsntaygtng gngcntgytt ygaymgnytn 1860
 ytncayccng aygngtncc ngcnytnnty mgnacngtnc cngtnnttyac nytncnwsn 1920
 carytnccng aytyytngg ngcnytnear carccnmng cncnmgnws nggnmgnytn 1980
 cargarmng cngarcargt nwsnmngcn ytncarccng cnytngayws ntayttyay 2040
 cncnggna cwnsngcncc nggnmgnggn gtnggncng gngcnggncc nggngcnggn 2100
 gaygnacn 2109

<210> 10
 <211> 2314
 <212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>

<221> CDS

<222> (199)..(2292)

<220>

<221> mat_peptide

<222> (259)..(2292)

<400> 10

```

ccaaatcgaa agcacgggag ctgatactgg gcctggagtc caggctcact ggagtgggga 60
agcatggctg gagaggaatt ctagcccttg ctctctccca gggacacggg gctgattgtc 120
agcagggggcg aggggtctgc ccccccttgg gggggcagga cggggcctca ggcctgggtg 180
ctgtccggca cctggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca 231
                Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala
                -20                               -15                -10

ctg ggc cga aac cct gtg gtc gtc tct ctg gag aga ctg atg gag cct 279
Leu Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro
                -5                               -1   1                5

cag gac act gca cgc tgc tct cta ggc ctc tcc tgc cac ctc tgg gat 327
Gln Asp Thr Ala Arg Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp
                10                               15                20

ggg gac gtg ctc tgc ctg cct gga agc ctc cag tct gcc cca ggc cct 375
Gly Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro
                25                               30                35

gtg cta gtg cct acc cgc ctg cag acg gag ctg gtg ctg agg tgt cca 423
Val Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro
                40                               45                50

cag aag aca gat tgc gcc ctc tgt gtc cgt gtg gtg gtc cac ttg gcc 471
Gln Lys Thr Asp Cys Ala Leu Cys Val Arg Val Val Val His Leu Ala
                60                               65                70

gtg cat ggg cac tgg gca gag cct gaa gaa gct gga aag tct gat tca 519
Val His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser
                75                               80                85

gaa ctc cag gag tct agg aac gcc tct ctc cag gcc cag gtg gtg ctc 567
Glu Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu
                90                               95                100

tcc ttc cag gcc tac ccc atc gcc cgc tgt gcc ctg ctg gag gtc cag 615
Ser Phe Gln Ala Tyr Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln
                105                               110                115

gtg ccc gct gac ctg gtg cag cct ggt cag tcc gtg ggt tct gcg gta 663
Val Pro Ala Asp Leu Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val
                120                               125                130                135

```

09063318 "0506301

ttt gac tgt ttc gag gct agt ctt ggg gct gag gta cag atc tgg tcc	711
Phe Asp Cys Phe Glu Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser	
140 145 150	
tac acg aag ccc agg tac cag aaa gag ctc aac ctc aca cag cag ctg	759
Tyr Thr Lys Pro Arg Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu	
155 160 165	
cct gac tgc agg ggt ctt gaa gtc cgg gac agc atc cag agc tgc tgg	807
Pro Asp Cys Arg Gly Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp	
170 175 180	
gtc ctg ccc tgg ctc aat gtg tct aca gat ggt gac aat gtc ctt ctg	855
Val Leu Pro Trp Leu Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu	
185 190 195	
aca ctg gat gtc tct gag gag cag gac ttt agc ttc tta ctg tac ctg	903
Thr Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu	
200 205 210 215	
cgt cca gtc ccg gat gct ctc aaa tcc ttg tgg tac aaa aac ctg act	951
Arg Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr	
220 225 230	
gga cct cag aac att act tta aac cac aca gac ctg gtt ccc tgc ctc	999
Gly Pro Gln Asn Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu	
235 240 245	
tgc att cag gtg tgg tcg cta gag cca gac tct gag agg gtc gaa ttc	1047
Cys Ile Gln Val Trp Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe	
250 255 260	
tgc ccc ttc cgg gaa gat ccc ggt gca cac agg aac ctc tgg cac ata	1095
Cys Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu Trp His Ile	
265 270 275	
gcc agg ctg cgg gta ctg tcc cca ggg gta tgg cag cta gat gcg cct	1143
Ala Arg Leu Arg Val Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro	
280 285 290 295	
tgc tgt ctg ccg ggc aag gta aca ctg tgc tgg cag gca cca gac cag	1191
Cys Cys Leu Pro Gly Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln	
300 305 310	
agt ccc tgc cag cca ctt gtg cca cca gtg ccc cag aag aac gcc act	1239
Ser Pro Cys Gln Pro Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr	
315 320 325	
gtg aat gag cca caa gat ttc cag ttg gtg gca ggc cac ccc aac ctc	1287
Val Asn Glu Pro Gln Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu	
330 335 340	
tgt gtc cag gtg agc acc tgg gag aag gtt cag ctg caa gcg tgc ttg	1335
Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu	
345 350 355	
tgg gct gac tcc ttg ggg ccc ttc aag gat gat atg ctg tta gtg gag	1383
Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu	
360 365 370 375	

09363818 053304

atg	aaa	acc	ggc	ctc	aac	aac	aca	tca	gtc	tgt	gcc	ttg	gaa	ccc	agt	1431
Met	Lys	Thr	Gly	Leu	Asn	Asn	Thr	Ser	Val	Cys	Ala	Leu	Glu	Pro	Ser	
				380					385					390		
ggc	tgt	aca	cca	ctg	ccc	agc	atg	gcc	tcc	acg	aga	gct	gct	cgc	ctg	1479
Gly	Cys	Thr	Pro	Leu	Pro	Ser	Met	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	
				395				400					405			
gga	gag	gag	ttg	ctg	caa	gac	ttc	cga	tca	cac	cag	tgt	atg	cag	ctg	1527
Gly	Glu	Glu	Leu	Leu	Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu	
			410				415					420				
tgg	aac	gat	gac	aac	atg	gga	tcg	cta	tgg	gcc	tgc	ccc	atg	gac	aag	1575
Trp	Asn	Asp	Asp	Asn	Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	
	425					430					435					
tac	atc	cac	agg	cgc	tgg	gtc	cta	gta	tgg	ctg	gcc	tgc	cta	ctc	ttg	1623
Tyr	Ile	His	Arg	Arg	Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	
	440				445					450					455	
gct	gcg	gcg	ctt	ttc	ttc	ttc	ctc	ctt	cta	aaa	aag	gac	cgc	agg	aaa	1671
Ala	Ala	Ala	Leu	Phe	Phe	Phe	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Arg	Lys	
				460				465						470		
gcg	gcc	cgt	ggc	tcc	cgc	acg	gcc	ttg	ctc	ctc	cac	tcc	gcc	gac	gga	1719
Ala	Ala	Arg	Gly	Ser	Arg	Thr	Ala	Leu	Leu	Leu	His	Ser	Ala	Asp	Gly	
				475				480					485			
gcg	ggc	tac	gag	cgc	ctg	gtg	gga	gca	ctg	gcg	tcc	gcg	ttg	agc	cag	1767
Ala	Gly	Tyr	Glu	Arg	Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Ser	Gln	
			490				495					500				
atg	cca	ctg	cgc	gtg	gcc	gtg	gac	ctg	tgg	agc	cgc	cgc	gag	ctg	agc	1815
Met	Pro	Leu	Arg	Val	Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	
	505					510					515					
gcg	cac	gga	gcc	cta	gcc	tgg	ttc	cac	cac	cag	cga	cgc	cgt	atc	ctg	1863
Ala	His	Gly	Ala	Leu	Ala	Trp	Phe	His	His	Gln	Arg	Arg	Arg	Ile	Leu	
	520				525					530					535	
cag	gag	ggt	ggc	gtg	gta	atc	ctt	ctc	ttc	tcg	ccc	gcg	gcc	gtg	gcg	1911
Gln	Glu	Gly	Gly	Val	Val	Ile	Leu	Leu	Phe	Ser	Pro	Ala	Ala	Val	Ala	
				540					545					550		
cag	tgt	cag	cag	tgg	ctg	cag	ctc	cag	aca	gtg	gag	ccc	ggg	ccg	cat	1959
Gln	Cys	Gln	Gln	Trp	Leu	Gln	Leu	Gln	Thr	Val	Glu	Pro	Gly	Pro	His	
				555				560					565			
gac	gcc	ctc	gcc	gcc	tgg	ctc	agc	tgc	gtg	cta	ccc	gat	ttc	ctg	caa	2007
Asp	Ala	Leu	Ala	Ala	Trp	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln	
				570			575					580				
ggc	cgg	gcg	acc	ggc	cgc	tac	gtc	ggg	gtc	tac	ttc	gac	ggg	ctg	ctg	2055
Gly	Arg	Ala	Thr	Gly	Arg	Tyr	Val	Gly	Val	Tyr	Phe	Asp	Gly	Leu	Leu	
	585					590					595					
cac	cca	gac	tct	gtg	ccc	tcc	ccg	ttc	cgc	gtc	gcc	ccg	ctc	ttc	tcc	2103
His	Pro	Asp	Ser	Val	Pro	Ser	Pro	Phe	Arg	Val	Ala	Pro	Leu	Phe	Ser	
	600				605					610					615	

09063843 "053301

```

ctg ccc tcg cag ctg ccg gct ttc ctg gat gca ctg cag gga ggc tgc 2151
Leu Pro Ser Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys
620 625 630

tcc act tcc gcg ggg cga ccc gcg gac cgg gtg gaa cga gtg acc cag 2199
Ser Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln
635 640 645

gcg ctg cgg tcc gcc ctg gac agc tgt act tct agc tcg gaa gcc cca 2247
Ala Leu Arg Ser Ala Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro
650 655 660

ggc tgc tgc gag gaa tgg gac ctg gga ccc tgc act aca cta gaa 2292
Gly Cys Cys Glu Glu Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
665 670 675

taaaagccga tacagtattc ct 2314

```

```

<210> 11
<211> 698
<212> PRT
<213> Unknown

```

```

<400> 11
Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Asn Pro
-20 -15 -10 -5

Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln Asp Thr Ala Arg
-1 1 5 10

Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly Asp Val Leu Cys
15 20 25

Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val Leu Val Pro Thr
30 35 40

Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln Lys Thr Asp Cys
45 50 55 60

Ala Leu Cys Val Arg Val Val Val His Leu Ala Val His Gly His Trp
65 70 75

Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu Leu Gln Glu Ser
80 85 90

Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr
95 100 105

Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val Pro Ala Asp Leu
110 115 120

Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe Asp Cys Phe Glu
125 130 135 140

Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr Thr Lys Pro Arg
145 150 155

Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro Asp Cys Arg Gly

```

"052201" 052201


```
<210> 12
<211> 2094
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(2094)
<223> n may be a, c, g, or t

<400> 12
atgccngtnw sntgggttyt nytnwsnytn gcnytnggnm gnaayccngt ngtnngtnwsn 60
ytnngarmgny tnatggarcc ncargayacn gcnmgntgyw snytnggnyb nwsntgycay 120
ytnntgggayg gngaygtnyt ntgyytnccn ggnwsnytn c arwsngcncc nggnccngtn 180
ytngtncnca cnmgnytnca racngarytn gtynytnmgnt gycncaraa racngaytgy 240
gcnytnatgyg tnmngntngt ngtncaaytn gcngtncaayg gncaytgggc ngarccngar 300
```

gargcnggna arwsngayws ngarytnear garwsnmgna aygcnwsnyt ncargencar 360
 gtngtnytnw snttycargc ntayccnath genmgntgyg cnytnytnga rgtncargtn 420
 ccngcngayy tngtnearcc nggncarwsn gtnggnwsng cngtnttyga ytgyttygar 480
 gcnwsnytnng gngcngargt ncarathtg wstnayacna arccnmgnta ycaraargar 540
 ytnaayyttna cncarcaryt nccngaytgy mgnggnytnng argtnmgnga ywsnathcar 600
 wsntgytggg tnytnccntg gytnaaygt nwsnacngayg gngayaaygt nytnytnacn 660
 ytngaygt nwsngargarca rgayttywsn tyytntnytn ayytnmgnc ngtnccngay 720
 gcnytnaarw snytnnggta yaaraayyt nccnggncnc araayathac nytnaaycay 780
 acngayytng tncntgyt ntgyathcar gtntggwsny tngarccnga ywsngarmgn 840
 gtngarttyt gyccnttyng ngargayccn ggngcncaym gnaayytntg gcayathgc 900
 mgnytnmgng tnytnwsncc ngngtntgg carytnngay cncntgytg yytnccnggn 960
 aargtnacny tntgytggca rgcncngay carwsnccnt gycarccnyt ngtnccncnc 1020
 gtncncara araaygcnc ngtnaaygar cncargayt tycarytngt ngcnggncay 1080
 ccnaayytnt gygtncargt nwsnacntgg garaargtnc arytnearc ntgytntgg 1140
 gcngaywsny tnggncntt yaargaygay atgytnytng tngaratgaa racnggnytn 1200
 aayaayacnw sngtntgygc nytngarccn wsnggntgya cncnytncc nwsnatggcn 1260
 wsnacmgng cngcnmgnyt ngngargar ytnytnearc ayttymgnws ncaycartgy 1320
 atgcarytnt ggaaygayga yaayatgggn wsnytnnggg cntgyccnat ggayaartay 1380
 athcaymgnm gntgggtnyt ngtnnggytn gentgyytn tnytnngcngc ngcnytnnt 1440
 tyytntny tnytnaaraa rgaymgnm aargcngcnm gggnwsnmg nacngcnytn 1500
 ytnytnayw sngcngaygg ngcngntay garmgnytn tnggngcnyt ngcnwsngcn 1560
 ytnwsncara tgccnytnmg ngtnngcngtn gayytnnggw snmgngnga rytnwsngcn 1620
 cayggngcny tngcntggtt ycaycaycar mgnmngmnga thytnearc rggngngtn 1680
 gtnathytny tnttywsncc ngcngcngtn gencartgy arcartggyt ncarytnear 1740
 acngtnearc cnggncncay ygaygcnytn gngcntgyg twnsntgygt nytnccngay 1800
 tyytnearc gnmngcnc nggngntay gtngngntnt aytygaygg nytnytnay 1860
 ccngaywsng tncnwsncc nttymgntn gncnytnnt tywsnytncc nwsncarytn 1920
 ccngcntty tngaygcnyt ncarggnggn tgywsnacnw sngcngngm nccngcngay 1980
 mgngtnearc gngtnacnc rgcnytnmg nwsngcnytn aywsntgyac nwsnwsnwsn 2040
 gargcncng gntgytgyga rgartgggay ytnngncnt gyacnacnyt ngar 2094

<400> 13																	
ccccgcgntc	cgggccagca	gcggggcggcc	ggggcgcgaga	gaacggcctg	gctggggcgag	60											
cgcacgggcc	atg	gcc	ccg	tgg	ctg	cag	ctc	tgc	tcc	gtc	ttc	ttt	acg	gtc	111		
Met		Ala	Pro	Trp	Leu	Gln	Leu	Cys	Ser	Val	Phe	Phe	Thr	Val			
-15				-10				-5									
aac	gcc	tgc	ctc	aac	ggc	tcg	cag	ctg	gct	gtg	gcc	gct	ggc	ggg	tcc	159	
Asn	Ala	Cys	Leu	Asn	Gly	Ser	Gln	Leu	Ala	Xaa	Ala	Ala	Gly	Gly	Ser		
-1		1		5				10									
ggc	cgc	gcg	cng	ggc	gcc	gac	acc	tgt	agc	tgg	ang	gga	gtg	ggg	cca	207	
Gly	Arg	Ala	Xaa	Gly	Ala	Asp	Thr	Cys	Ser	Trp	Xaa	Gly	Val	Gly	Pro		
15		20				25				30							
gcc	agc	aga	aac	agt	ggg	ctg	tac	aac	atc	acc	ttc	aaa	tat	gac	aat	255	
Ala	Ser	Arg	Asn	Ser	Gly	Leu	Tyr	Asn	Ile	Thr	Phe	Lys	Tyr	Asp	Asn		
35				40				45									
tgt	acc	acc	tac	ttg	aat	cca	gtg	ggg	aag	cat	gtg	att	gct	gac	gcc	303	
Cys	Thr	Thr	Tyr	Leu	Asn	Pro	Val	Gly	Lys	His	Val	Ile	Ala	Asp	Ala		
50			55				60										
cag	aat	atc	acc	atc	agc	cag	tat	gct	tgc	cat	gac	caa	gtg	gca	gtc	351	
Gln	Asn	Ile	Thr	Ile	Ser	Gln	Tyr	Ala	Cys	His	Asp	Gln	Val	Ala	Val		
65			70				75										
acc	att	ctt	tgg	tcc	cca	ggg	gcc	ctc	ggc	atc	gaa	ttc	ctg	aaa	gga	399	
Thr	Ile	Leu	Trp	Ser	Pro	Gly	Ala	Leu	Gly	Ile	Glu	Phe	Leu	Lys	Gly		
80		85				90											
ttt	cgg	gta	ata	ctg	gag	gag	ctg	aag	tcg	gag	gga	aga	cag	ngc	caa	447	
Phe	Arg	Val	Ile	Leu	Glu	Glu	Leu	Lys	Ser	Glu	Gly	Arg	Gln	Xaa	Gln		
95		100				105				110							
caa	ctg	att	cta	aag	gat	ccg	aag	cag	ntc	aac	agt	agc	ttc	aaa	aga	495	

Gln	Leu	Ile	Leu	Lys	Asp	Pro	Lys	Gln	Xaa	Asn	Ser	Ser	Phe	Lys	Arg	
				115					120					125		
act	gga	atg	gaa	tct	caa	cct	ttn	ctg	aat	atg	aaa	ttt	gaa	acg	gat	543
Thr	Gly	Met	Glu	Ser	Gln	Pro	Xaa	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp	
			130					135					140			
tat	ttc	gta	agg	ttg	tcc	ttt	tcc	ttc	att	aaa	aac	gaa	agc	aat	tac	591
Tyr	Phe	Val	Arg	Leu	Ser	Phe	Ser	Phe	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	
		145					150					155				
cac	cct	ttc	ttc	ttt	aga	acc	cga	gcc	tgt	gac	ctg	ttg	tta	cag	ccg	639
His	Pro	Phe	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro	
	160					165					170					
gac	aat	cta	gct	tgt	aaa	ccc	ttc	tgg	aag	cct	cgg	aac	ctg	aac	atc	687
Asp	Asn	Leu	Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile	
175					180					185					190	
agc	cag	cat	ggc	tcg	gac	atg	cag	gtg	tcc	ttc	gac	cac	gca	ccg	cac	735
Ser	Gln	His	Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His	
				195				200					205			
aac	ttc	ggc	ttc	cgt	ttc	ttc	tat	ctt	cac	tac	aag	ctc	aag	cac	gaa	783
Asn	Phe	Gly	Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	Lys	Leu	Lys	His	Glu	
			210				215					220				
gga	cct	ttc	aag	cga	aag	acc	tgt	aag	cag	gag	caa	act	aca	gag	atg	831
Gly	Pro	Phe	Lys	Arg	Lys	Thr	Cys	Lys	Gln	Glu	Gln	Thr	Thr	Glu	Met	
		225				230						235				
acc	agc	tgc	ctc	ctt	caa	aat	gtt	tct	cca	ggg	gat	tat	ata	att	gag	879
Thr	Ser	Cys	Leu	Leu	Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu	
	240					245					250					
ctg	gtg	gat	gac	act	aac	aca	aca	aga	aaa	gtg	atg	cat	tat	gcc	tta	927
Leu	Val	Asp	Asp	Thr	Asn	Thr	Thr	Arg	Lys	Val	Met	His	Tyr	Ala	Leu	
255					260					265					270	
aag	cca	gtg	cac	tcc	ccg	tgg	gcc	ggg	ccc	atc	aga	gcc	gtg	gcc	atc	975
Lys	Pro	Val	His	Ser	Pro	Trp	Ala	Gly	Pro	Ile	Arg	Ala	Val	Ala	Ile	
				275				280					285			
aca	gtg	cca	ctg	gta	gtc	ata	tcg	gca	ttc	gcg	acg	ctc	ttc	act	gtg	1023
Thr	Val	Pro	Leu	Val	Val	Ile	Ser	Ala	Phe	Ala	Thr	Leu	Phe	Thr	Val	
		290					295					300				
atg	tgc	cgc	aag	aag	caa	caa	gaa	aat	ata	tat	tca	cat	tta	gat	gaa	1071
Met	Cys	Arg	Lys	Lys	Gln	Gln	Glu	Asn	Ile	Tyr	Ser	His	Leu	Asp	Glu	
		305				310						315				
gag	agc	tct	gag	tct	tcc	aca	tac	act	gca	gca	ctc	cca	aga	gag	agg	1119
Glu	Ser	Ser	Glu	Ser	Ser	Thr	Tyr	Thr	Ala	Ala	Leu	Pro	Arg	Glu		

Gln	Asn	His	Met	Asn	Val	Val	Gln	Cys	Phe	Ala	Tyr	Phe	Leu	Gln	Asp		
				355					360					365			
ttc	tgt	ggc	tgt	gag	gtg	gct	ctg	gac	ctg	tgg	gaa	gac	ttc	agc	ctc	1263	
Phe	Cys	Gly	Cys	Glu	Val	Ala	Leu	Asp	Leu	Trp	Glu	Asp	Phe	Ser	Leu		
			370					375					380				
tgt	aga	gaa	ggg	cag	aga	gaa	tgg	gtc	atc	cag	aag	atc	cac	gag	tcc	1311	
Cys	Arg	Glu	Gly	Gln	Arg	Glu	Trp	Val	Ile	Gln	Lys	Ile	His	Glu	Ser		
		385					390					395					
cag	ttc	atc	att	gtg	gtt	tgt	tcc	aaa	ggg	atg	aag	tac	ttt	gtg	gac	1359	
Gln	Phe	Ile	Ile	Val	Val	Cys	Ser	Lys	Gly	Met	Lys	Tyr	Phe	Val	Asp		
	400					405					410						
aag	aag	aac	tac	aaa	cac	aaa	gga	ggg	ggc	cga	ggc	tcg	ggg	aaa	gga	1407	
Lys	Lys	Asn	Tyr	Lys	His	Lys	Gly	Gly	Gly	Arg	Gly	Ser	Gly	Lys	Gly		
415					420					425					430		
gag	ctc	ttc	ctg	gtg	gcg	gtg	tca	gcc	att	gcc	gaa	aag	ctc	cgc	cag	1455	
Glu	Leu	Phe	Leu	Val	Ala	Val	Ser	Ala	Ile	Ala	Glu	Lys	Leu	Arg	Gln		
				435				440						445			
gcc	aag	cag	agt	tcg	tcc	gcg	gcg	ctc	agc	aag	ttt	atc	gcc	gtc	tac	1503	
Ala	Lys	Gln	Ser	Ser	Ser	Ala	Ala	Leu	Ser	Lys	Phe	Ile	Ala	Val	Tyr		
			450					455					460				
ttt	gat	tat	tcc	tgc	gag	gga	gac	gtc	ccc	ggg	atc	cta	gac	ctg	agt	1551	
Phe	Asp	Tyr	Ser	Cys	Glu	Gly	Asp	Val	Pro	Gly	Ile	Leu	Asp	Leu	Ser		
		465				470					475						
acc	aag	tac	aga	ctc	atg	gac	aat	ctt	cct	cag	ctc	tgt	tcc	cac	ctg	1599	
Thr	Lys	Tyr	Arg	Leu	Met	Asp	Asn	Leu	Pro	Gln	Leu	Cys	Ser	His	Leu		
	480					485					490						
cac	tcc	cga	gac	cac	ggc	ctc	cag	gag	ccg	ggg	cag	cac	acg	cga	cag	1647	
His	Ser	Arg	Asp	His	Gly	Leu	Gln	Glu	Pro	Gly	Gln	His	Thr	Arg	Gln		
495					500					505					510		
ggc	agc	aga	agg	aac	tac	ttc	cgg	agc	aag	tca	ggc	cgg	tcc	cta	tac	1695	
Gly	Ser	Arg	Arg	Asn	Tyr	Phe	Arg	Ser	Lys	Ser	Gly	Arg	Ser	Leu	Tyr		
				515					520					525			
gtc	gcc	att	tgc	aac	atg	cac	cag	ttt	att	gac	gag	gag	ccc	gac	tgg	1743	
Val	Ala	Ile	Cys	Asn	Met	His	Gln	Phe	Ile	Asp	Glu	Glu	Pro	Asp	Trp		
			530					535					540				
ttc	gaa	aag	cag	ttc	gtt	ccc	ttc	cat	cct	cct	cca	ctg	cgc	tac	cgg	1791	
Phe	Glu	Lys	Gln	Phe	Val	Pro	Phe	His	Pro	Pro	Pro	Leu	Arg	Tyr	Arg		
		545					550					555					
gag	cca	gtc	ttg	gag	aaa	ttt	gat	tcg	ggc	ttg	gtt	tta	aat	gat	gtc	1839	
Glu	Pro	Val	Leu	Glu	Lys	Phe	Asp	Ser	Gly	Leu	Val	Leu	Asn	Asp	Val		
	560					565					570						
atg	tgc	aaa	cca	ggg	cct	gag	agt	gac	ttc	tgc	cta	aag	gta	gag	gcg	1887	
Met	Cys	Lys	Pro	Gly	Pro	Glu	Ser	Asp	Phe	Cys	Leu	Lys	Val	Glu	Ala		
575					580					585					590		
gct	gtt	ctt	ggg	gca	acc	gga	cca	gcc	gac	tcc	cag	cac	gag	agt	cag	1935	

09664 0544

Ala	Val	Leu	Gly	Ala	Thr	Gly	Pro	Ala	Asp	Ser	Gln	His	Glu	Ser	Gln	
				595					600					605		
cat	ggg	ggc	ctg	gac	caa	gac	ggg	gag	gcc	cgg	cct	gcc	ctt	gac	ggc	1983
His	Gly	Gly	Leu	Asp	Gln	Asp	Gly	Glu	Ala	Arg	Pro	Ala	Leu	Asp	Gly	
			610					615					620			
agc	gcc	gcc	ctg	caa	ccc	ctg	ctg	cac	acg	gtg	aaa	gcc	ggc	agc	ccc	2031
Ser	Ala	Ala	Leu	Gln	Pro	Leu	Leu	His	Thr	Val	Lys	Ala	Gly	Ser	Pro	
			625				630					635				
tcg	gac	atg	ccg	cgg	gac	tca	ggc	atc	tat	gac	tcg	tct	gtg	ccc	tca	2079
Ser	Asp	Met	Pro	Arg	Asp	Ser	Gly	Ile	Tyr	Asp	Ser	Ser	Val	Pro	Ser	
			640				645					650				
tcc	gag	ctg	tct	ctg	cca	ctg	atg	gaa	gga	ctc	tcg	acg	gac	cag	aca	2127
Ser	Glu	Leu	Ser	Leu	Pro	Leu	Met	Glu	Gly	Leu	Ser	Thr	Asp	Gln	Thr	
					660					665					670	
gaa	acg	tct	tcc	ctg	acg	gag	agc	gtg	tcc	tcc	tct	tca	ggc	ctg	ggc	2175
Glu	Thr	Ser	Ser	Leu	Thr	Glu	Ser	Val	Ser	Ser	Ser	Ser	Gly	Leu	Gly	
				675				680						685		
gag	gag	gaa	cct	cct	gcc	ctt	cct	tcc	aag	ctc	ctc	tct	tct	ggg	tca	2223
Glu	Glu	Glu	Pro	Pro	Ala	Leu	Pro	Ser	Lys	Leu	Leu	Ser	Ser	Gly	Ser	
			690					695					700			
tgc	aaa	gca	gat	ctt	ggc	tgc	cgc	agc	tac	act	gat	gaa	ctc	cac	gcg	2271
Cys	Lys	Ala	Asp	Leu	Gly	Cys	Arg	Ser	Tyr	Thr	Asp	Glu	Leu	His	Ala	
			705				710					715				
gtc	gcc	cct	ttg	taacaaaacg	aaagagtcta	agcattgcc	ctttagctgc									2323
Val	Ala	Pro	Leu													
			720													
tgccctccctc	tgattcccca	gctcatctcc	ctgggtgcat	ggcccacttg	gagctgaggt											2383
ctcatacaag	gatatttgga	gtgaaatgct	ggccagtact	tgttctccct	tgccccaacc											2443
ctttaccgga	tatcttgaca	aactctccaa	ttttctaaaa	tgatatggag	ctctgaaagg											2503
catgtccata	aggtctgaca	acagcttgcc	aaatttggtt	agtccttgga	tcagagcctg											2563
ttgtgggagg	tagggaggaa	atatgtaaag	aaaaacagga	agatacctgc	actaatcatt											2623
cagacttcat	tgagctctgc	aaactttgcc	tgtttgctat	tggttacctt	gatttgaaat											2683
gctttgtgaa	aaaaggcact	tttaacatca	tagccacaga	aatcaagtgc	cagtctatct											2743
ggaatccatg	ttgtattgca	gataatgttc	tcatttattt	ttg												2786
<210>	14															
<211>	738															
<212>	PRT															
<213>	Unknown															
<400>	14															
Met	Ala	Pro	Trp	Leu	Gln	Leu	Cys	Ser	Val	Phe	Phe	Thr	Val	Asn	Ala	
	-15					-10					-5					

Cys 1	Leu	Asn	Gly	Ser 5	Gln	Leu	Ala	Xaa	Ala 10	Ala	Gly	Gly	Ser	Gly 15	Arg
Ala	Xaa	Gly	Ala 20	Asp	Thr	Cys	Ser	Trp 25	Xaa	Gly	Val	Gly	Pro 30	Ala	Ser
Arg	Asn 35	Ser	Gly	Leu	Tyr	Asn 40	Ile	Thr	Phe	Lys	Tyr 45	Asp	Asn	Cys	Thr
Thr	Tyr 50	Leu	Asn	Pro	Val	Gly 55	Lys	His	Val	Ile	Ala 60	Asp	Ala	Gln	Asn
Ile 65	Thr	Ile	Ser	Gln 70	Tyr	Ala	Cys	His	Asp	Gln 75	Val	Ala	Val	Thr	Ile 80
Leu	Trp	Ser	Pro	Gly 85	Ala	Leu	Gly	Ile	Glu 90	Phe	Leu	Lys	Gly	Phe 95	Arg
Val	Ile	Leu	Glu 100	Glu	Leu	Lys	Ser	Glu 105	Gly	Arg	Gln	Xaa	Gln 110	Gln	Leu
Ile	Leu 115	Lys	Asp	Pro	Lys	Gln 120	Xaa	Asn	Ser	Ser	Phe	Lys 125	Arg	Thr	Gly
Met 130	Glu	Ser	Gln	Pro	Xaa	Leu 135	Asn	Met	Lys	Phe	Glu 140	Thr	Asp	Tyr	Phe
Val 145	Arg	Leu	Ser	Phe 150	Ser	Phe	Ile	Lys	Asn 155	Glu	Ser	Asn	Tyr	His	Pro 160
Phe	Phe	Phe	Arg 165	Thr	Arg	Ala	Cys	Asp	Leu 170	Leu	Leu	Gln	Pro	Asp 175	Asn
Leu	Ala	Cys	Lys 180	Pro	Phe	Trp	Lys	Pro 185	Arg	Asn	Leu	Asn	Ile 190	Ser	Gln
His	Gly 195	Ser	Asp	Met	Gln	Val	Ser 200	Phe	Asp	His	Ala 205	Pro	His	Asn	Phe
Gly 210	Phe	Arg	Phe	Phe	Tyr	Leu 215	His	Tyr	Lys	Leu	Lys 220	His	Glu	Gly	Pro
Phe 225	Lys	Arg	Lys	Thr 230	Cys	Lys	Gln	Glu	Gln 235	Thr	Thr	Glu	Met	Thr	Ser 240
Cys	Leu	Leu	Gln 245	Asn	Val	Ser	Pro	Gly	Asp 250	Tyr	Ile	Ile	Glu	Leu 255	Val
Asp	Asp	Thr 260	Asn	Thr	Thr	Arg	Lys	Val 265	Met	His	Tyr	Ala	Leu 270	Lys	Pro
Val	His 275	Ser	Pro	Trp	Ala	Gly 280	Pro	Ile	Arg	Ala	Val	Ala 285	Ile	Thr	Val
Pro 290	Leu	Val	Val	Ile	Ser	Ala 295	Phe	Ala	Thr	Leu	Phe 300	Thr	Val	Met	Cys
Arg 305	Lys	Lys	Gln	Gln 310	Glu	Asn	Ile	Tyr	Ser	His 315	Leu	Asp	Glu	Glu	Ser 320

Ser	Glu	Ser	Ser	Thr	Tyr	Thr	Ala	Ala	Leu	Pro	Arg	Glu	Arg	Leu	Arg
				325					330					335	
Pro	Arg	Pro	Lys	Val	Phe	Leu	Cys	Tyr	Ser	Ser	Lys	Asp	Gly	Gln	Asn
			340					345					350		
His	Met	Asn	Val	Val	Gln	Cys	Phe	Ala	Tyr	Phe	Leu	Gln	Asp	Phe	Cys
		355					360					365			
Gly	Cys	Glu	Val	Ala	Leu	Asp	Leu	Trp	Glu	Asp	Phe	Ser	Leu	Cys	Arg
	370					375					380				
Glu	Gly	Gln	Arg	Glu	Trp	Val	Ile	Gln	Lys	Ile	His	Glu	Ser	Gln	Phe
385					390					395					400
Ile	Ile	Val	Val	Cys	Ser	Lys	Gly	Met	Lys	Tyr	Phe	Val	Asp	Lys	Lys
				405					410					415	
Asn	Tyr	Lys	His	Lys	Gly	Gly	Gly	Arg	Gly	Ser	Gly	Lys	Gly	Glu	Leu
			420					425					430		
Phe	Leu	Val	Ala	Val	Ser	Ala	Ile	Ala	Glu	Lys	Leu	Arg	Gln	Ala	Lys
		435					440					445			
Gln	Ser	Ser	Ser	Ala	Ala	Leu	Ser	Lys	Phe	Ile	Ala	Val	Tyr	Phe	Asp
	450					455					460				
Tyr	Ser	Cys	Glu	Gly	Asp	Val	Pro	Gly	Ile	Leu	Asp	Leu	Ser	Thr	Lys
465					470					475					480
Tyr	Arg	Leu	Met	Asp	Asn	Leu	Pro	Gln	Leu	Cys	Ser	His	Leu	His	Ser
				485					490					495	
Arg	Asp	His	Gly	Leu	Gln	Glu	Pro	Gly	Gln	His	Thr	Arg	Gln	Gly	Ser
			500					505					510		
Arg	Arg	Asn	Tyr	Phe	Arg	Ser	Lys	Ser	Gly	Arg	Ser	Leu	Tyr	Val	Ala
		515					520					525			
Ile	Cys	Asn	Met	His	Gln	Phe	Ile	Asp	Glu	Glu	Pro	Asp	Trp	Phe	Glu
	530					535					540				
Lys	Gln	Phe	Val	Pro	Phe	His	Pro	Pro	Pro	Leu	Arg	Tyr	Arg	Glu	Pro
545					550					555					560
Val	Leu	Glu	Lys	Phe	Asp	Ser	Gly	Leu	Val	Leu	Asn	Asp	Val	Met	Cys
				565					570					575	
Lys	Pro	Gly	Pro	Glu	Ser	Asp	Phe	Cys	Leu	Lys	Val	Glu	Ala	Ala	Val
			580					585					590		
Leu	Gly	Ala	Thr	Gly	Pro	Ala	Asp	Ser	Gln	His	Glu	Ser	Gln	His	Gly
		595					600					605			
Gly	Leu	Asp	Gln	Asp	Gly	Glu	Ala	Arg	Pro	Ala	Leu	Asp	Gly	Ser	Ala
	610					615					620				
Ala	Leu	Gln	Pro	Leu	Leu	His	Thr	Val	Lys	Ala	Gly	Ser	Pro	Ser	Asp
625					630					635					640

Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu
645 650 655

Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr
660 665 670

Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu
675 680 685

Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys
690 695 700

Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala
705 710 715 720

Pro Leu

<210> 15
<211> 2214
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(2214)
<223> n may be a, c, g, or t

<400> 15
atggcncnt ggytncaryt ntgywsngtn ttyttyacng tnaaygcntg yytnaayggn 60
wsncarytng cngtngcngc ngnggnwnsn ggnmgngcnn nnggngcnga yacntgywsn 120
tggnnngng tnggnccngc nwsnmgnaay wsnggnytn tayaayathac nttyaartay 180
gayaaytgay cnacntayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay 240
athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn 300
ggngcnytn gnatgarrt yytnaarggn ttmngntna thytngarga rytnaarwsn 360
gargngmgnc arnnncarca rytathyt nargayccna arcarnnnaa ywsnwsntty 420
aarmgnacng gnatggarws ncarccnnnn ytnaayatga arttygarac ngaytaytty 480
gtngnytnw snttywsntt yathaaraay garwsnaayt aycayccntt ytytytmgn 540
acnmngcngt gygayytnyt nytnarccn gayaayytn cngyaaarcc nttytggaar 600
ccnmgnaayy tnaayathws ncarcayggn wsngaytgc argtnwsntt ygaycaygcn 660
ccncayaayt tyggnttymg nttytytay ytncaytaya arytnaarca ygargngccn 720
ttyaarmgna arantgyaa rcargarcar acnacngara tgacnwsntg ytnytnar 780
aaygtwnsnc cngngayta yathathgar ytnngngayg ayacnaayac nacnmgnaar 840
gtnatgcayt aygnytnaa rccngtnca ywsncntggg cnggnccnat hmgngcngtn 900

0586345 0586345

```
<210> 16
<211> 2012
<212> DNA
<213> Unknown
```

```
<220>
<221> CDS
<222> (1) .. (1971)
<220>
```

<221> mat_peptide
 <222> (70)..(1971)

<400> 16

atg ggg agc tcc aga ctg gca gcc ctg ctc ctg cct ctc ctc ctc ata	48
Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile	
-20 -15 -10	
gtc atc gac ctc tct gac tct gct ggg att ggc ttt cgc cac ctg ccc	96
Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro	
-5 -1 1 5	
cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct	144
His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro	
10 15 20 25	
ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt	192
Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly	
30 35 40	
gtg tgc gag tct ggc act gtt ccc gct gtt tgt gcc agc atc tgc tgt	240
Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys	
45 50 55	
cag gtg gct cag gtc ttc aac ggg gcc tct tcc acc tcc tgg tgc aga	288
Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg	
60 65 70	
aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc	336
Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys	
75 80 85	
cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga	384
Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg	
90 95 100 105	
aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac	432
Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp	
110 115 120	
ttc gct cta aaa gga ccc aac ctt cgg atc cag aga cat ggg aaa gtc	480
Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val	
125 130 135	
ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac	528
Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn	
140 145 150	
agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg	576
Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu	
155 160 165	
ctg cct gag gcc cgg gct att cgg gtg acc ata tct tca ggc cct gag	624
Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu	
170 175 180 185	
gtc agc gtg cgt ctt tgt cac cag tgg gca ctg gag tgt gaa gag ctg	672
Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu	
190 195 200	

09863848 052304

agc Ser	agt Ser	ccc Pro	tat Tyr 205	gat Asp	gtc Val	cag Gln	aaa Lys	att Ile 210	gtg Val	tct Ser	ggg Gly	ggc Gly	cac His 215	act Thr	gta Val	720
gag Glu	ctg Leu	cct Pro 220	tat Tyr	gaa Glu	ttc Phe	ctt Leu	ctg Leu 225	ccc Pro	tgt Cys	ctg Leu	tgc Cys	ata Ile 230	gag Glu	gca Ala	tcc Ser	768
tac Tyr	ctg Leu 235	caa Gln	gag Glu	gac Asp	act Thr	gtg Val 240	agg Arg	cgc Arg	aaa Lys	aaa Lys	tgt Cys 245	ccc Pro	ttc Phe	cag Gln	agc Ser	816
tgg Trp 250	cca Pro	gaa Glu	gcc Ala	tat Tyr	ggc Gly 255	tgc Ser	gac Asp	ttc Phe	tgg Trp	aag Lys 260	tca Ser	gtg Val	cac His	ttc Phe	act Thr 265	864
gac Asp	tac Tyr	agc Ser	cag Gln	cac His 270	act Thr	cag Gln	atg Met	gtc Val	atg Met 275	gcc Ala	ctg Leu	aca Thr	ctc Leu	cgc Arg 280	tgc Cys	912
cca Pro	ctg Leu	aag Lys 285	ctg Leu	gaa Glu	gct Ala	gcc Ala	ctc Leu	tgc Cys 290	cag Gln	agg Arg	cac His	gac Asp	tgg Trp 295	cat His	acc Thr	960
ctt Leu	tgc Cys	aaa Lys 300	gac Asp	ctc Leu	ccg Pro	aat Asn 305	gcc Ala	acg Thr	gct Ala	cga Arg	gag Glu	tca Ser 310	gat Asp	ggg Gly	tgg Trp	1008
tat Tyr	gtt Val 315	ttg Leu	gag Glu	aag Lys	gtg Val 320	gac Asp	ctg Leu	cac His	ccc Pro	cag Gln	ctc Leu 325	tgc Cys	ttc Phe	aag Lys	gta Val	1056
caa Gln 330	cca Pro	tgg Trp	ttc Phe	tct Ser	ttt Phe 335	gga Gly	aac Asn	agc Ser	agc Ser	cat His 340	gtt Val	gaa Glu	tgc Cys	ccc Pro	cac His 345	1104
cag Gln	act Thr	ggg Gly	tct Ser	ctc Leu 350	aca Thr	tcc Ser	tgg Trp	aat Asn 355	gta Val	agc Ser	atg Met	gat Asp	acc Thr	caa Gln 360	gcc Ala	1152
cag Gln	cag Gln	ctg Leu	att Ile 365	ctt Leu	cac His	ttc Phe	tcc Ser	tca Ser 370	aga Arg	atg Met	cat His	gcc Ala	acc Thr 375	ttc Phe	agt Ser	1200
gct Ala	gcc Ala	tgg Trp 380	agc Ser	ctc Leu	cca Pro	ggc Gly	ttg Leu 385	ggg Gly	cag Gln	gac Asp	act Thr	ttg Leu 390	gtg Val	ccc Pro	ccc Pro	1248
gtg Val	tac Tyr 395	act Thr	gtc Val	agc Ser	cag Gln	gtg Val 400	tgg Trp	cgg Arg	tca Ser	gat Asp	gtc Val 405	cag Gln	ttt Phe	gcc Ala	tgg Trp	1296
aag Lys 410	cac His	ctc Leu	ttg Leu	tgt Cys	cca Pro 415	gat Asp	gtc Val	tct Ser	tac Tyr	aga Arg 420	cac His	ctg Leu	ggg Gly	ctc Leu	ttg Leu 425	1344
atc Ile	ctg Leu	gca Ala	ctg Leu 430	ctg Leu	gcc Ala	ctc Leu	ctc Leu	acc Thr 435	cta Leu	ctg Leu	ggt Gly	gtt Val	gtt Val	ctg Leu 440	gcc Ala	1392

```
<210> 17
<211> 657
<212> PRT
<213> Unknown
```

<400> 17
Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile
 -20 -15 -10

Val	Ile	Asp	Leu	Ser	Asp	Ser	Ala	Gly	Ile	Gly	Phe	Arg	His	Leu	Pro
		-5				-1	1				5				
His	Trp	Asn	Thr	Arg	Cys	Pro	Leu	Ala	Ser	His	Thr	Glu	Val	Leu	Pro
10					15					20					25
Ile	Ser	Leu	Ala	Ala	Pro	Gly	Gly	Pro	Ser	Ser	Pro	Gln	Ser	Leu	Gly
				30					35					40	
Val	Cys	Glu	Ser	Gly	Thr	Val	Pro	Ala	Val	Cys	Ala	Ser	Ile	Cys	Cys
			45					50					55		
Gln	Val	Ala	Gln	Val	Phe	Asn	Gly	Ala	Ser	Ser	Thr	Ser	Trp	Cys	Arg
		60					65					70			
Asn	Pro	Lys	Ser	Leu	Pro	His	Ser	Ser	Ser	Ile	Gly	Asp	Thr	Arg	Cys
	75					80					85				
Gln	His	Leu	Leu	Arg	Gly	Ser	Cys	Cys	Leu	Val	Val	Thr	Cys	Leu	Arg
90					95					100					105
Arg	Ala	Ile	Thr	Phe	Pro	Ser	Pro	Pro	Gln	Thr	Ser	Pro	Thr	Arg	Asp
				110					115					120	
Phe	Ala	Leu	Lys	Gly	Pro	Asn	Leu	Arg	Ile	Gln	Arg	His	Gly	Lys	Val
			125					130					135		
Phe	Pro	Asp	Trp	Thr	His	Lys	Gly	Met	Glu	Val	Gly	Thr	Gly	Tyr	Asn
		140					145					150			
Arg	Arg	Trp	Val	Gln	Leu	Ser	Gly	Gly	Pro	Glu	Phe	Ser	Phe	Asp	Leu
	155					160					165				
Leu	Pro	Glu	Ala	Arg	Ala	Ile	Arg	Val	Thr	Ile	Ser	Ser	Gly	Pro	Glu
170					175					180					185
Val	Ser	Val	Arg	Leu	Cys	His	Gln	Trp	Ala	Leu	Glu	Cys	Glu	Glu	Leu
				190					195					200	
Ser	Ser	Pro	Tyr	Asp	Val	Gln	Lys	Ile	Val	Ser	Gly	Gly	His	Thr	Val
			205					210					215		
Glu	Leu	Pro	Tyr	Glu	Phe	Leu	Leu	Pro	Cys	Leu	Cys	Ile	Glu	Ala	Ser
		220					225					230			
Tyr	Leu	Gln	Glu	Asp	Thr	Val	Arg	Arg	Lys	Lys	Cys	Pro	Phe	Gln	Ser
	235					240					245				
Trp	Pro	Glu	Ala	Tyr	Gly	Ser	Asp	Phe	Trp	Lys	Ser	Val	His	Phe	Thr
250					255					260					265
Asp	Tyr	Ser	Gln	His	Thr	Gln	Met	Val	Met	Ala	Leu	Thr	Leu	Arg	Cys
				270					275					280	
Pro	Leu	Lys	Leu	Glu	Ala	Ala	Leu	Cys	Gln	Arg	His	Asp	Trp	His	Thr
			285					290					295		
Leu	Cys	Lys	Asp	Leu	Pro	Asn	Ala	Thr	Ala	Arg	Glu	Ser	Asp	Gly	Trp
		300					305					310			

Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
 315 320 325
 Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
 330 335 340 345
 Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
 350 355 360
 Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
 365 370 375
 Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
 380 385 390
 Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
 395 400 405
 Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
 410 415 420 425
 Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
 430 435 440
 Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
 445 450 455
 Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
 460 465 470
 Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
 475 480 485
 Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
 490 495 500 505
 Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
 510 515 520
 Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
 525 530 535
 Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
 540 545 550
 Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
 555 560 565
 Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
 570 575 580 585
 Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
 590 595 600
 Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
 605 610 615
 Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
 620 625 630

09863313 "056301

Gly

<210> 18
 <211> 1971
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(1971)
 <223> n may be a, c, g, or t

<400> 18
 atgggnwsnw snmgnytngc ngcnytnytn ytnccnytny tnytnathgt nathgayytn 60
 wsngaywsng cnggnathgg nttymgncay ytnccncayt ggaayacnmg ntgyccnytn 120
 gcnwsncaya cngargtnyt nccnathwsn ytngcngcnc cnggnggncc nwsnwsnccn 180
 carwsnytnng gngtntgyga rwsnggnacn gtncngcng tntgygcnws nathtgytgy 240
 cargtngcnc argtnttyaa yggngcnwsn wsnacnwsnt ggtgymgnaa yccnaarwsn 300
 ytnccncayw snwsnwsnat hggngayacn mgntgyarc ayytnytnmg nggnwsntgy 360
 tgyytngtng tnacntgyyt nmgnmgngcn athacnttyc cnwsnccncc ncaracnwsn 420
 ccnacnmng aytytgynt naarggnccn ayytnmgna thcarmgna yggnaargtn 480
 ttyccngayt ggacncayaa rggnatggar gtnggnacng gntayaaymg nmgtgggtn 540
 carytnwsng gnggnccnga rtytwsntty gayytnytn cngargcnmg ngcnathmgn 600
 gtnacnathw snwsnggncc ngargtnwsn gtnmgnytn gycaycartg ggcnytngar 660
 tgygargary tnwsnwsncc ntaygaygtn caraarathg tnwsngngng ncayacngtn 720
 garytnccnt aygarttyt nytnccntgy ytntgyathg argcnwsnta yytnccargar 780
 gayacngtnm gnmgnaaraa rtgyccntty carwsntggc cngargcnta yggnwsngay 840
 ttytggaarw sngtncaytt yacngaytay wsncarcaya cncaratggt natggcnytn 900
 acnytnmgnt gyccnytnaa rytngargcn gcnytnntgyc armgncayga ytggcayacn 960
 ytntgyaarg ayytnccnaa ygcnacngcn mgngarwsng ayggntggta ygtnytngar 1020
 aargtngayy tncayccnca rytntgytty aargtnarc cntggtytws nttyggnaay 1080
 wsnwsncayg tngartgycc ncaycaracn ggnwsnytna cnwsntggaa ygtnwsnatg 1140
 gayacncarg cncarcaryt nathytnca ytywsnwsnm gnatgcaygc nacnttywsn 1200
 gcngcntggw snytnccngg nytnngncar gayacnytn tncnccngt ntayacngtn 1260
 wsnargtnt ggmgnwsnga ygtncartty gcntggaarc ayytnytntg yccngaygtn 1320

05263316 "05263316"

wsntaymgnc ayytnggny tnytnathytn gcnytnytn gnytnytnac nytnytnngn 1380
gtngtnytn gnytnacntg ymgngmgnccn carwsnggnc cnggncncgc nmgnccngtn 1440
ytynytnytn aygcngcnga ywsngargcn carmgngmny tngtnggngc nytnngcgar 1500
ytynytnmgng cngcnytnng nggnggngmgn gaygtathg tngayytnng ggarggngmgn 1560
caygtngcnm gngtnggnc nytnccntgg ytntgggngc cnmgncnmg ngtngcnmgn 1620
garcarggna cngtnytnytn nytnnggwsn ggngcngayy tnmgnccngt nwsnggncn 1680
gayccnmng cngcncnytn nytnngcnytn ytncaygng cncnmgnc nytnytnytn 1740
ytngcntayt tywsnmgnytn ntgygcnar ggngayathc cncncncnytn nmngcnytn 1800
ccnmngntaym gnytnytnmg ngayytnccn mgnytnytnm gngcnytna ygcnmgnccn 1860
ttygcngarg cnacwsntg gggngmnytn ggngcnmgnc armngmgnca rwsnmgnytn 1920
garytnngyw snmgnytna rmngargcn gcnmgnytn cngayytnng n 1971

<210> 19
<211> 808
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>
<221> CDS
<222> (78)..(806)

<220>
<221> mat_peptide
<222> (147)..(806)

<400> 19
cagctccggg ccagccctg ctgccctctt gcagacagga aagacatggt ctctgcgcc 60

tgatcctaca gaagctc atg ggg agc ccc aga ctg gca gcc ttg ctc ctg 110
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
-20 -15

tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc 158
Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
-10 -5 -1 1

tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt 206
Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg
5 10 15 20

gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg 254
Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu
25 30 35

gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac 302

09263918 052304

Val	Arg	Lys	Ser	Lys	Ser	Pro	Pro	Lys	Phe	Glu	Asp	Tyr	Trp	Arg	His		
			40					45					50				
agg	aca	cca	gca	tcc	ttc	cag	agg	aag	ctg	cta	ggc	agc	cct	tcc	ctg	350	
Arg	Thr	Pro	Ala	Ser	Phe	Gln	Arg	Lys	Leu	Leu	Gly	Ser	Pro	Ser	Leu		
		55					60				65						
tct	gag	gaa	agc	cat	cga	att	tcc	atc	ccc	tcc	tca	gcc	atc	tcc	cac	398	
Ser	Glu	Glu	Ser	His	Arg	Ile	Ser	Ile	Pro	Ser	Ser	Ala	Ile	Ser	His		
	70					75				80							
aga	ggc	caa	cgc	acc	aaa	agg	gcc	cag	cct	tca	gct	gca	gaa	gga	aga	446	
Arg	Gly	Gln	Arg	Thr	Lys	Arg	Ala	Gln	Pro	Ser	Ala	Ala	Glu	Gly	Arg		
	85				90				95						100		
gaa	cat	ctc	cct	gaa	gca	ggg	tca	caa	aag	tgt	gga	gga	cct	gaa	ttc	494	
Glu	His	Leu	Pro	Glu	Ala	Gly	Ser	Gln	Lys	Cys	Gly	Gly	Pro	Glu	Phe		
				105				110						115			
tcc	ttt	gat	ttg	ctg	ccc	gag	gtg	cag	gct	gtt	cgg	gtg	act	att	cct	542	
Ser	Phe	Asp	Leu	Leu	Pro	Glu	Val	Gln	Ala	Val	Arg	Val	Thr	Ile	Pro		
			120					125					130				
gca	ggc	ccc	aag	gca	cgt	gtg	cgc	ctt	tgt	tat	cag	tgg	gca	ctg	gaa	590	
Ala	Gly	Pro	Lys	Ala	Arg	Val	Arg	Leu	Cys	Tyr	Gln	Trp	Ala	Leu	Glu		
		135				140						145					
tgt	gaa	gac	ttg	agt	agc	cct	ttt	gat	acc	cag	aaa	att	gtg	tct	gga	638	
Cys	Glu	Asp	Leu	Ser	Ser	Pro	Phe	Asp	Thr	Gln	Lys	Ile	Val	Ser	Gly		
	150					155				160							
ggg	cac	act	gta	gac	ctg	cct	tat	gaa	ttc	ctt	ctg	ccc	tgc	atg	tgc	686	
Gly	His	Thr	Val	Asp	Leu	Pro	Tyr	Glu	Phe	Leu	Leu	Pro	Cys	Met	Cys		
	165				170					175					180		
ata	gag	gcc	tcc	tac	ctg	caa	gag	gac	act	gtg	agg	cgc	aaa	agt	gtc	734	
Ile	Glu	Ala	Ser	Tyr	Leu	Gln	Glu	Asp	Thr	Val	Arg	Arg	Lys	Ser	Val		
				185					190					195			
cct	tcc	aga	gct	ggc	ctg	aag	ctt	atg	gct	cag	act	tct	ggc	agt	caa	782	
Pro	Ser	Arg	Ala	Gly	Leu	Lys	Leu	Met	Ala	Gln	Thr	Ser	Gly	Ser	Gln		
			200				205						210				
tac	gct	tca	ctg	act	aca	gcc	agc	ac								808	
Tyr	Ala	Ser	Leu	Thr	Thr	Ala	Ser										
		215				220											
<210>	20																
<211>	243																
<212>	PRT																
<213>	Unknown																
<400>	20																
Met	Gly	Ser	Pro	Arg	Leu	Ala	Ala	Leu	Leu	Leu	Ser	Leu	Pro	Leu	Leu		
			-20					-15					-10				
Leu	Ile	Gly	Leu	Ala	Val	Ser	Ala	Arg	Val	Ala	Cys	Pro	Cys	Leu	Arg		
	-5					-1	1				5						

09063818 "0523301"

Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
 10 15 20 25
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 30 35 40
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
 45 50 55
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
 60 65 70
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
 75 80 85
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
 90 95 100 105
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
 110 115 120
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
 125 130 135
 Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
 140 145 150
 Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
 155 160 165
 Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
 170 175 180 185
 Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val Pro Ser Arg Ala Gly
 190 195 200
 Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln Tyr Ala Ser Leu Thr
 205 210 215
 Thr Ala Ser
 220

<210> 21
 <211> 729
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(729)
 <223> n may be a, c, g, or t

<400> 21
 atgggnwsnc cnmgnytngc ngcnytnytn ytnwsnytn cnytnytnytn nathggnytn 60
 gcngtnwsng cnmgngtngc ntgyccntgy ytnmgwnsnt ggacnwsnca ytggytnytn 120
 gentaymgng tngayaarmg nttygcnggn ytn cartggg gntgggttycc nytnytnytn 180

09030301

mgnaarwsna arwsnccncc naarttygar gaytaytggm gncaymgnac nccngcnwsn 240
 ttycarmgna arytnytngg nwsnccnwsn ytnwsngarg arwsncaymg nathwsnath 300
 ccnwsnwsng cnathwsnca ymgnggncar mgnacnaarm gngcncarcc nwsngengcn 360
 garggnmgng arcayytnc ngargcnggn wsncaraart gyggnggncc ngarttywsn 420
 ttygayytny tncengargt ncargcngtn mgngtnacna thccngcngg nccnaargcn 480
 mgngtnmgny tntgytayca rtgggcnyn gartgygarg ayytnwsnws nccnttygay 540
 acncaraara thgtnwsngg nggncayacn gtngayytnc cntaygartt yytnytncn 600
 tgyatgtgya thgargcnws ntayytncar gargayacng tnmgnmgnaa rwsngtnccn 660
 wsnmgngcng gnytnaaryt natggcncar acnwsnggnw sncartaygc nwsnytnacn 720
 acngcnwsn 729

<210> 22
 <211> 2377
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (180)..(1874)

<400> 22
 ttttgagcag aggccttccta ggctccgtag aaatttgcat acagcttcca cttcctgctt 60
 cagagcctgt tcttctactt acctgggccc ggagaaggtg gagggagacg agaagccgcc 120
 gagagccgac taccctccgg gccagctctg tctgtccgtg gtggatctaa gaaactaga 179
 atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca 227
 Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
 1 5 10 15
 agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca 275
 Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
 20 25 30
 gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct 323
 Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
 35 40 45
 gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac 371
 Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
 50 55 60
 tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc 419
 Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
 65 70 75 80

090304 0304

acc	tgc	ctg	cgc	act	caa	gtt	ctg	gag	gac	agt	gaa	gac	agt	ttc	tgc	467
Thr	Cys	Leu	Arg	Thr	Gln	Val	Leu	Glu	Asp	Ser	Glu	Asp	Ser	Phe	Cys	
				85					90				95			
agg	aga	cac	cca	ggc	ctg	ggc	aaa	gct	ttc	cct	tct	ggg	tgc	tct	gca	515
Arg	Arg	His	Pro	Gly	Leu	Gly	Lys	Ala	Phe	Pro	Ser	Gly	Cys	Ser	Ala	
				100					105				110			
gtc	agc	gag	cct	gcg	tct	gag	tct	gtg	gtt	gga	gcc	ctc	cct	gca	gag	563
Val	Ser	Glu	Pro	Ala	Ser	Glu	Ser	Val	Val	Gly	Ala	Leu	Pro	Ala	Glu	
				115					120				125			
cat	cag	ttt	tca	ttt	atg	gaa	aaa	cgt	aat	caa	tgg	ctg	gta	tct	cag	611
His	Gln	Phe	Ser	Phe	Met	Glu	Lys	Arg	Asn	Gln	Trp	Leu	Val	Ser	Gln	
				130					135				140			
ctt	tca	gcg	gct	tct	cct	gac	act	ggc	cat	gac	tca	gac	aaa	tca	gac	659
Leu	Ser	Ala	Ala	Ser	Pro	Asp	Thr	Gly	His	Asp	Ser	Asp	Lys	Ser	Asp	
				145					150				155			
caa	agt	tta	cct	aat	gcc	tca	gca	gac	tcc	ttg	ggc	ggt	agc	cag	gag	707
Gln	Ser	Leu	Pro	Asn	Ala	Ser	Ala	Asp	Ser	Leu	Gly	Gly	Ser	Gln	Glu	
				165					170				175			
atg	gtg	caa	cgg	ccc	cag	cct	cac	agg	aac	cga	gca	ggc	ctg	gat	ctg	755
Met	Val	Gln	Arg	Pro	Gln	Pro	His	Arg	Asn	Arg	Ala	Gly	Leu	Asp	Leu	
				180					185				190			
cca	acc	ata	gac	acg	gga	tat	gat	tcc	cag	ccc	cag	gat	gtc	ctg	ggc	803
Pro	Thr	Ile	Asp	Thr	Gly	Tyr	Asp	Ser	Gln	Pro	Gln	Asp	Val	Leu	Gly	
				195					200				205			
atc	agg	cag	ctg	gaa	agg	ccc	ctg	ccc	ctc	acc	tcc	gtg	tgt	tac	ccc	851
Ile	Arg	Gln	Leu	Glu	Arg	Pro	Leu	Pro	Leu	Thr	Ser	Val	Cys	Tyr	Pro	
				210					215				220			
cag	gac	ctc	ccc	aga	cct	ctc	agg	tcc	agg	gag	ttc	cct	cag	ttt	gaa	899
Gln	Asp	Leu	Pro	Arg	Pro	Leu	Arg	Ser	Arg	Glu	Phe	Pro	Gln	Phe	Glu	
				225					230				235			
cct	cag	agg	tat	cca	gca	tgt	gca	cag	atg	ctg	cct	ccc	aat	ctt	tcc	947
Pro	Gln	Arg	Tyr	Pro	Ala	Cys	Ala	Gln	Met	Leu	Pro	Pro	Asn	Leu	Ser	
				245					250				255			
cca	cat	gct	cca	tgg	aac	tat	cat	tac	cat	tgt	cct	gga	agt	ccc	gat	995
Pro	His	Ala	Pro	Trp	Asn	Tyr	His	Tyr	His	Cys	Pro	Gly	Ser	Pro	Asp	
				260					265				270			
cac	cag	gtg	cca	tat	ggc	cat	gac	tac	cct	cga	gca	gcc	tac	cag	caa	1043
His	Gln	Val	Pro	Tyr	Gly	His	Asp	Tyr	Pro	Arg	Ala	Ala	Tyr	Gln	Gln	
				275					280				285			
gtg	atc	cag	ccg	gct	ctg	cct	ggg	cag	ccc	ctg	cct	gga	gcc	agt	gtg	1091
Val	Ile	Gln	Pro	Ala	Leu	Pro	Gly	Gln	Pro	Leu	Pro	Gly	Ala	Ser	Val	
				290					295				300			
aga	ggc	ctg	cac	cct	gtg	cag	aag	gtt	atc	ctg	aat	tat	ccc	agc	ccc	1139
Arg	Gly	Leu	His	Pro	Val	Gln	Lys	Val	Ile	Leu	Asn	Tyr	Pro	Ser	Pro	
				305					310				315			
												320				

tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg	1187
Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly	
325 330 335	
ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct	1235
Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala	
340 345 350	
ggg gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag	1283
Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln	
355 360 365	
gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac	1331
Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn	
370 375 380	
cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg	1379
Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu	
385 390 395 400	
cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg	1427
Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val	
405 410 415	
aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac	1475
Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp	
420 425 430	
ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag	1523
Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu	
435 440 445	
cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc	1571
Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro	
450 455 460	
aaa tac aaa cag gac gtg gaa ggc gct gag tcg cag ctg gac gag gat	1619
Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp	
465 470 475 480	
gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag	1667
Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu	
485 490 495	
ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc	1715
Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe	
500 505 510	
cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat	1763
Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His	
515 520 525	
gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg	1811
Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu	
530 535 540	
aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt	1859
Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu	
545 550 555 560	

Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
165 170 175

Met	Val	Gln	Arg 180	Pro	Gln	Pro	His	Arg 185	Asn	Arg	Ala	Gly	Leu 190	Asp	Leu
Pro	Thr	Ile 195	Asp	Thr	Gly	Tyr	Asp 200	Ser	Gln	Pro	Gln	Asp 205	Val	Leu	Gly
Ile	Arg 210	Gln	Leu	Glu	Arg	Pro 215	Leu	Pro	Leu	Thr	Ser 220	Val	Cys	Tyr	Pro
Gln 225	Asp	Leu	Pro	Arg	Pro 230	Leu	Arg	Ser	Arg	Glu 235	Phe	Pro	Gln	Phe	Glu 240
Pro	Gln	Arg	Tyr	Pro 245	Ala	Cys	Ala	Gln	Met 250	Leu	Pro	Pro	Asn	Leu 255	Ser
Pro	His	Ala	Pro 260	Trp	Asn	Tyr	His	Tyr 265	His	Cys	Pro	Gly	Ser 270	Pro	Asp
His	Gln	Val 275	Pro	Tyr	Gly	His	Asp 280	Tyr	Pro	Arg	Ala	Ala 285	Tyr	Gln	Gln
Val 290	Ile	Gln	Pro	Ala	Leu	Pro 295	Gly	Gln	Pro	Leu	Pro 300	Gly	Ala	Ser	Val
Arg 305	Gly	Leu	His	Pro	Val 310	Gln	Lys	Val	Ile	Leu 315	Asn	Tyr	Pro	Ser	Pro 320
Trp	Asp	Gln	Glu 325	Glu	Arg	Pro	Ala	Gln	Arg 330	Asp	Cys	Ser	Phe	Pro 335	Gly
Leu	Pro	Arg	His 340	Gln	Asp	Gln	Pro	His 345	His	Gln	Pro	Pro	Asn 350	Arg	Ala
Gly	Ala	Pro 355	Gly	Glu	Ser	Leu	Glu 360	Cys	Pro	Ala	Glu	Leu 365	Arg	Pro	Gln
Val 370	Pro	Gln	Pro	Pro	Ser	Pro 375	Ala	Ala	Val	Pro	Arg 380	Pro	Pro	Ser	Asn
Pro 385	Pro	Ala	Arg	Gly	Thr	Leu	Lys	Thr	Ser	Asn 395	Leu	Pro	Glu	Glu	Leu 400
Arg	Lys	Val	Phe 405	Ile	Thr	Tyr	Ser	Met	Asp 410	Thr	Ala	Met	Glu	Val 415	Val
Lys	Phe	Val	Asn 420	Phe	Leu	Leu	Val	Asn 425	Gly	Phe	Gln	Thr	Ala 430	Ile	Asp
Ile	Phe	Glu 435	Asp	Arg	Ile	Arg	Gly 440	Ile	Asp	Ile	Ile	Lys 445	Trp	Met	Glu
Arg	Tyr 450	Leu	Arg	Asp	Lys	Thr 455	Val	Met	Ile	Ile	Val 460	Ala	Ile	Ser	Pro
Lys 465	Tyr	Lys	Gln	Asp	Val 470	Glu	Gly	Ala	Glu	Ser 475	Gln	Leu	Asp	Glu	Asp 480
Glu	His	Gly	Leu	His 485	Thr	Lys	Tyr	Ile	His 490	Arg	Met	Met	Gln	Ile 495	Glu

Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
 500 505 510
 Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
 515 520 525
 Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
 530 535 540
 Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
 545 550 555 560
 Gln Val Val Pro Leu
 565

<210> 24
 <211> 1695
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(1695)
 <223> n may be a, c, g, or t

<400> 24
 atgaaymgw snathccngt ngargtngay garwsngarc cntayccnws ncarytnytn 60
 aarccnathc cngartayws nccngargar garwsngarc cncngcncnc naayathmgn 120
 aayatggcnc cnaaywsnyt nwsngcncnc acnatgytnc ayaaywsnws nggngaytty 180
 wsnrcargcnc aywsnacnyt naarytngcn aaycaycarm gncngtnws nmgnrcargtn 240
 acntgyytnm gnacncargt nytngargay wsngargayw snttytgymg nmgnrcayccn 300
 ggnytnngna argcnttycc nwsnggntgy wsngcngtnw sngarccngc nwsngarwsn 360
 gtngtnngng cnytnccngc ngarcaycar ttywsnttya tggaraarmg naaycartgg 420
 ytngtnwsnc arytnwsngc ngcnwsnccn gayacnggnc aygaywsnga yaarwsngay 480
 carwsnytnc cnaaygcnws ngcngaywsn ytngngngnw sncargarat ggtncarmgn 540
 ccncarcnc aymgnaaymg ngcnggnytn gayytnccna cnathgayac nggntaygay 600
 wsnrcarcnc argaygtnyt nggnathmgn carytngarm gncnytncc nytnacnwsn 660
 gtntgytayc cncargayyt nccnmgnccn ytnmgnwsnm gngarttycc ncarttygar 720
 ccncarmgnt ayccngcntg ygcncaratg ytnccncna ayytnwsncc ncaygcncnc 780
 tggaaytayc aytaycaytg yccnggnwsn ccngaycayc argtnccnta yggncaygay 840
 tayccnmngng cngcntayca rcargtnath carccngcny tncnggnca rccnytnccn 900
 ggngcnwsng tnmnggnytn ncayccngtn caraargtna thytnaayta yccnwsnccn 960

05363318 "05363318"

tgggaycarg argarmgncc ngencarmgn gaytgywsnt tyccnggnyt nccnmgncaay 1020
 cargaycarc cncaycayca rccnccnaay mgngcnggng cncnggnga rwsnytngar 1080
 tgyccngcng arytnmgnc ncartnccn carccnccnw snccngcngc ngtnccnmgn 1140
 cccnccwsna ayccnccngc nmngggnaen ytnaaracnw snaayytnc ngargarytn 1200
 mgnaargtnt tyathacnta ywsnatggay acngcnatgg argtngtnaa rttygtnaay 1260
 ttyytnytng tnaayggntt ycaracngcn athgayatht tygargaymg nathmgnggn 1320
 athgayatha thaartggat ggarmgntay ytnmgngaya aracngtnat gathathgtn 1380
 gcnathwsnc cnaartayaa rcargaygtn gargngcng arwsncaryt ngaygargay 1440
 garcayggny tncayacnaa rtayathcay mgnatgatgc arathgartt yathaarc 1500
 ggnwsnatga ayttymgntt yathccngtn ytnttyccna aygcnaaraa rgarcaygtn 1560
 ccnactggy tncaraayac ncaygtntay wsntggccna araayaaraa raayathytn 1620
 ytnmgnytny tnmnggarga rgartaygtn gcncnccnm gnggncnnyt nccnacnytn 1680
 cargtngtnc cnytn 1695

<210> 25

<211> 1323

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>

<221> CDS

<222> (1)..(1026)

<400> 25

cag gac ctc cct ggg cct ctg agg tcc agg gaa ttg cca cct cag ttt 48
 Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe

1 5 10 15

gaa ctt gag agg tat cca atg aac gcc cag ctg ctg ccg ccc cat cct 96
 Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro

20 25 30

tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc 144
 Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro

35 40 45

tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc 192
 Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala

50 55 60

tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg 240
 Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly

65 70 75 80

gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac	288
Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp	
85 90 95	
tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct	336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser	
100 105 110	
ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga	384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly	
115 120 125	
gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca	432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro	
130 135 140	
cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc	480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser	
145 150 155 160	
aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa	528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu	
165 170 175	
tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg	576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val	
180 185 190	
gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att	624
Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile	
195 200 205	
gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg	672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met	
210 215 220	
gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc	720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser	
225 230 235 240	
ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag	768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu	
245 250 255	
gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att	816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile	
260 265 270	
gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc	864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu	
275 280 285	
ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act	912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr	
290 295 300	
cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg	960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu	
305 310 315 320	

09863818-052301

ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc 1008
 Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
 325 330 335

ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc 1056
 Leu Gln Val Val Pro Leu
 340

ctgtttctcac agcattcttc tagcggagct ggctggtggc acccaggccc tggaacacct 1116

cttctacaga gtcctctgtc tcttgagtct gagttgtcct cgctgggctt ccagagcttc 1176

agtgcctgga tgctgcaggt gacagaaaca aacatctatg accacaaaaa ctctcatcac 1236

ttcagctact tttatgagtc ggtcagatgc tctgtgtcct tagaccagtc taaatcatgc 1296

tcaaataata aaatgattat tctttgt 1323

<210> 26

<211> 342

<212> PRT

<213> Unknown

<400> 26

Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe
 1 5 10 15

Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
 20 25 30

Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
 35 40 45

Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
 50 55 60

Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
 65 70 75 80

Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
 85 90 95

Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
 100 105 110

Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
 115 120 125

Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
 130 135 140

His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
 145 150 155 160

Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
 165 170 175

Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val

09063418 052301

180 185 190
 Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile
 195 200 205
 Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met
 210 215 220
 Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser
 225 230 235 240
 Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu
 245 250 255
 Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile
 260 265 270
 Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu
 275 280 285
 Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr
 290 295 300
 His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu
 305 310 315 320
 Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
 325 330 335
 Leu Gln Val Val Pro Leu
 340

<210> 27
 <211> 1026
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(1026)
 <223> n amy be a, c, g, or t

<400> 27
 cargayytnc cnggnccnyt nmgnwsnmgn garytnccnc cncarttyga rytngarmgn 60
 tayccnatga aygcncaryt nytnccnccn cayccnwsnc cncargcncc ntggaaytgy 120
 cartaytayt gycngngngg nccntaycay caycargtnc cncayggnga yggntayccn 180
 ccngcngcng cntaycarca rgtnytnear ccngcnytn cnggncargt nytnccnggn 240
 gcnmgngcnm gnggnccnmg nccngtnear aargtnathy tnaaygayws nwsnccncar 300
 gaycargarg armgnccngc ncarmnggay ttywsnttyc cnmgnytncc nmnggaycar 360
 yntaymgnc cncnwsnaa yggngtngar gcncngarg arwsnytnga yytnccngcn 420
 garytnmgnc cncayggnc ncargcnccn wsnytnngcng cngtnccnmg nccnccnwsn 480

```
<210> 28
<211> 207
<212> PRT
<213> Unknown
```

<400> 28

Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln
145 150 155 160

Glu Ala Val Leu Arg Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp
195 200 205

```
<220>
<223> Description of Unknown Organism:worm; surmised
      Caenorabditis elegans
```

```

4400> 31
Phe Lys Val Met Leu Val Cys Pro Glu Val Ser Gly Arg Asp Glu Asp
1           5           10           15

```

Val Cys Asp Arg Trp Phe Glu Asp Ser Lys Asn Ala Glu Glu Asn Met
35 40 45

Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile
65 70 75 80

Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu
85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu
100 105 110

Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala
115 120 125

Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu
130 135 140

Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn
145 150 155 160

Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser
165 170 175

Asn Ser